

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: April 7, 2004, 16:59:33 ; Search time 52.9316 Seconds
(without alignments)
1362.959 Million cell updates/sec

Title: US-09-195-368-1_COPY_48_177
Perfect score: 694
Sequence: 1 FLOETAKPCMAKFGPLPS.....VLKNNTYWGIIILNPOFIS 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 27475446 residues
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCAI=200 -THR.SCORE=PCT -THR.MAX=100 -THR.MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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5: /cg2_6/ptodata/2/ina/PTUS.COMB.seq:
6: /cg2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	694	100.0	1849	2	US-08-912-227-1 Sequence 1, Appli
2	694	100.0	1849	4	US-09-513-584-1 Sequence 1, Appli
3	694	100.0	1849	4	US-09-345-790-1 Sequence 1, Appli
4	84.5	12.2	3666	4	US-09-107-532A-305 Sequence 305, App
5	83.5	12.0	1008	4	US-09-354-138-130 Sequence 130, App
6	77	11.1	8543	3	US-08-496-944-1 Sequence 1, Appli
7	74.5	10.7	699	3	US-08-998-416-717 Sequence 717, App
8	74	10.7	935	6	US-08-998-416-717 Patent No. 5182196
9	74	10.7	2240	3	US-08-697-610-1 Sequence 1, Appli
10	74	10.7	2240	3	US-08-349-357-1 Sequence 1, Appli
11	74	10.7	2339	4	US-09-645-926A-6 Sequence 6, Appli
12	74	10.7	2359	5	PCT-US95-16980-1 Sequence 1, Appli

13	74	10.7	2455	4	US-09-167-109-3 Sequence 3, Appli
14	74	10.7	2925	4	US-09-540-236-384 Sequence 384, App
15	74	10.7	99629	4	US-09-596-002-37 Sequence 37, Appli
16	71.5	10.3	663	3	US-08-998-416-847 Sequence 847, App
17	71.5	10.3	705	3	US-08-998-416-831 Sequence 831, App
18	71.5	10.3	709	3	US-08-998-416-865 Sequence 865, App
19	71.5	10.3	741	3	US-08-998-416-869 Sequence 869, App
20	71.5	10.3	3650	4	US-09-620-312D-30 Sequence 30, Appli
21	71	10.2	465	4	US-09-604-694B-2 Sequence 2, Appli
22	71	10.2	471	1	US-08-538-875-2 Sequence 2, Appli
23	71	10.2	660	6	5182196-1 Patent No. 5182196
24	71	10.2	699	2	US-08-394-600B-1 Sequence 1, Appli
25	71	10.2	699	2	US-08-888-999A-1 Sequence 1, Appli
26	71	10.2	699	2	US-08-230-428B-1 Sequence 1, Appli
27	71	10.2	699	4	US-09-156-163A-1 Sequence 1, Appli
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31	71	10.2	699	5	PCT-US95-02513-1 Sequence 1, Appli
32	71	10.2	699	5	3422425-1 Patent No. 3422425
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36	71	10.2	947	2	US-08-184-009-89 Sequence 89, Appli
37	71	10.2	947	2	US-08-458-356-89 Sequence 89, Appli
38	71	10.2	947	3	US-08-460-736-89 Sequence 89, Appli
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41	71	10.2	965	2	US-08-458-356-79 Sequence 79, Appli
42	71	10.2	965	3	US-08-460-736-79 Sequence 79, Appli
43	71	10.2	965	4	US-09-535-370-79 Sequence 79, Appli
44	71	10.2	1100	4	US-09-589-287B-1 Sequence 1, Appli
45	71	10.2	1100	4	US-09-588-947A-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-912-227-1
Sequence 1, Application US/08912227
Patent No. 5998171
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Nt, Jian
TITLE OF INVENTION: Human Endokine Alpha
TITLE OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,227
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,058
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1486.0470001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 53..559
US-08-912-227-1

Alignment Scores:
Pred. No.: 3,1e-91 Length: 1849
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x US-08-912-227-1 (1-1849)

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DB 170 TTTCTCCAAATTAGAGCTGTAGAGAGCCCTGTATGCTTAAGTTTGACCATTAACCTCA 229

QY 21 LysTPGlnMetAlaserseercluprocysvalasnlvsaseraspTlyseu 40
DB 230 AATGGCAATGGCACTCTTGAAGCTCTTGCGTAAGCTCTGACTGGAAGCTG 289

QY 41 GlulleuglnasnnglyleuTyrlleuTyrglyglnvalalaproasnlaasntyr 60
DB 290 GAGATACCTTCAGAAATGGCTTATATTATATGCGCAAGTGGCTCCCAATGCCAAGTAC 349

QY 61 AsnAspValAlaProPheGlnValArgLeuTyrlsAsnlyAspMetIleGlnThrleu 80
DB 350 AATGATGATGCTCTTTTGAAGTGGCTGTATTAATAAACAAGACATGATCAAACTCTA 409

QY 81 ThrAsnlyseerlyleGlnasnValGlyGlyThrTyrglnleuHisValGlyAspThr 100
DB 410 ACAAAACAATCTTAATAATCCAAAATGAGAGGACTTATGAATTCAGTGGGACACC 469

QY 101 IleAspLeuIlePheasnserGluHsglnValleuIleAsnAspThrTyTPGlyIle 120
DB 470 ATGACTTGATTAATCACTGAGCATCAGGTTCTTAATAAATAAATACCTACTGGGATAC 529

QY 121 IleleuLeuAlaasnProGlnPheIleSer 130
DB 530 ATTTACTAGCAATCCCAATTCATCTCC 559

RESULT 2
US-09-513-584-1
Sequence 1, Application US/09513584
Patent No. 6406867
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endocrine Alpha and Methods
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESLER, GOLDSTEIN & FOX,
ADDRESSER: P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/513,584
FILING DATE: 25-FEB-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,058
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,227
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/122,099
FILING DATE: 26-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/136,788
FILING DATE: 28-MAY-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/345,790
FILING DATE: 01-JUL-1999
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0470005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 53..559
US-09-513-584-1

Alignment Scores:
Pred. No.: 3,1e-91 Length: 1849
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x US-09-513-584-1 (1-1849)

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QY 21 LysTPGlnMetAlaserseercluprocysvalasnlvsaseraspTlyseu 40
DB 230 AATGGCAATGGCACTCTTGAAGCTCTTGCGTAAGCTCTGACTGGAAGCTG 289

QY 41 GlulleuglnasnnglyleuTyrlleuTyrglyglnvalalaproasnlaasntyr 60
DB 290 GAGATACCTTCAGAAATGGCTTATATTATATGCGCAAGTGGCTCCCAATGCCAAGTAC 349

QY 61 AsnAspValAlaProPheGlnValArgLeuTyrlsAsnlyAspMetIleGlnThrleu 80
DB 350 AATGATGATGCTCTTTTGAAGTGGCTGTATTAATAAACAAGACATGATCAAACTCTA 409

QY 81 ThrAsnlyseerlyleGlnasnValGlyGlyThrTyrglnleuHisValGlyAspThr 100
DB 410 ACAAAACAATCTTAATAATCCAAAATGAGAGGACTTATGAATTCAGTGGGACACC 469

QY 101 IleAspLeuIlePheasnserGluHsglnValleuIleAsnAspThrTyTPGlyIle 120
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RESULT 3
US-09-345-790-1
/ Sequence 1, Application US/09345790
/ Patent No. 6521742
/ GENERAL INFORMATION:
/ APPLICANT: Yu, Guo-Liang
/ APPLICANT: Ni, Jian
/ APPLICANT: Rosen, Craig A.
/ TITLE OF INVENTION: Human Endokine Alpha
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
/ STREET: 1100 NEW YORK AVE., NW, SUITE 600
/ CITY: WASHINGTON
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/345,790
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/912,227
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Steffe, Eric K.
/ REGISTRATION NUMBER: 36,688
/ REFERENCE/DOCKET NUMBER: 1488.0470001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-371-2600
/ TELEFAX: 202-371-2540
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1849 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 53..559
US-09-345-790-1

Alignment Scores:
Pred. No.: 3,1e-91 Length: 1849
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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QY      21  Lys1rpg1nMe1a1a5e1r5e1rG1uP1rOCy5Va1a5n1y5Va15e1rAsp1r1y151eu 40
Db      230  AAAAGGCAATGGCATCTTCTGAACCTCCTGGCTGAATPAAGGTCTGACTGGAGCTG 289
QY      41  G1u11e1eug1n1a5nG1y11e1u1y1r1e1u11e1y1rG1y1G1n1v1a1a1P1ro5a5n1a1a5n1Ty1r 60
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QY      81  ThrAsnLysSerLysIleGlnAsnValAlaGlyThrTYrGluLeuHISValIGLYAspThr 100
Db      410  ACAAAACAATCTTAAATCCAAAATGAGAGGACTTATGAATTGATGTGTGGGGACACC 469
QY      101  ILAspLeuIlePheAsnSerGluHISGlnValIleuLysAsnAsnThrTYrTPGlyIle 120
Db      470  ATGACTGTATTCATTCACACTGTGAGCATCAGGTCTTAAAAATAATACCTACTGGGGATAC 529
QY      121  ILeuLeuValIAsnProGlnPheIleSer 130
Db      530  ATTTTACTAGCAATCCCAATTCATCTCC 559

RESULT 4
US-09-107-532A-305
; Sequence 305, Application US/09107532A
; Patent No. 658375
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS: THERAPEUTICS CORPORATION
; ADDRESSEE: GENOME
; STREET: 100 Beaver Street
; CITY: Walham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arimello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 305:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3666 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1..3666
; SEQUENCE DESCRIPTION: SEQ ID NO: 305:
US-09-107-532A-305

Alignment Scores:
Pred. No.: 0.142 Length: 3666
Score: 84.50 Matches: 19

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Percent Similarity: 57.58% Conservative: 19
 Best Local Similarity: 28.79% Mismatches: 23
 Query Match: 12.18% Indels: 5
 DB: 4 Gaps: 1

US-09-195-368-1_COPY_48_177 (1-130) x US-09-107-532A-305 (1-3666)

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 QY 75 AspMetIleGlnThrLeuThrAsnLysSer-----LysIleGlnAspVal 89
 DB 1603 AATGTTACTACCAAGAACCAATAGAAATCCACAGGTTCTGTAGAAATGAAAGATA 1662
 QY 90 GtlyGlyThrTyGluLeuHisValAlGlyAspThrIleAspLeuIlePheAsnSerGluHis 109
 DB 1663 GCGCATTTAGATGAGTACGACTACCGAATGAGTATTCACGATTTATATCCGATAC 1722
 QY 110 GlnValLeuLYeAsnAsn 115
 DB 1723 AAAGTTGTAAGAAATAC 1740

RESULT 5
 US-09-354-138-130

/ Sequence 130, Application US/09354138

/ Patent No. 6309647

/ GENERAL INFORMATION:

/ APPLICANT: Paolucci, Enzo

/ APPLICANT: Tartaglia, James

/ APPLICANT: Taylor, Jill

/ APPLICANT: Gettig, Russell

/ TITLE OF INVENTION: FOXYVIRUS - CANINE DISTEMPER VIRUS (CDV)

/ TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE

/ NUMBER OF SEQUENCES: 139

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Curtis, Morris & Safford, P.C.

/ STREET: 530 Fifth Avenue, 25th Floor

/ CITY: New York

/ STATE: New York

/ COUNTRY: United States of America

/ ZIP: 10036

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/354.138

/ FILING DATE:

/ CLASSIFICATION:

/ APPLICATION NUMBER: US 08/472,379

/ FILING DATE: 07-JUN-1995

/ APPLICATION NUMBER: US 08/416,646

/ FILING DATE: 05-APR-1995

/ APPLICATION NUMBER: US 08/224,657

/ FILING DATE: 16-APR-1994

/ APPLICATION DATA:

/ APPLICATION NUMBER: US 08/073,962

/ FILING DATE: 08-JUN-1993

/ APPLICATION DATA:

/ APPLICATION NUMBER: US 07/776,867

/ FILING DATE: 23-OCT-1991

/ APPLICATION DATA:

/ APPLICATION NUMBER: US 07/621,614

/ FILING DATE: 30-NOV-1990

/ APPLICATION DATA:

/ APPLICATION NUMBER: US 07/938,283

/ FILING DATE: 31-AUG-1993

/ APPLICATION DATA:

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/105,483

/ FILING DATE: 12-AUG-1993

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/847,951

/ FILING DATE: 06-MAR-1992

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 07/713,967

/ FILING DATE: 11-JUN-1991

/ APPLICATION DATA:

/ APPLICATION NUMBER: US 07,666,056

/ FILING DATE: 07-MAR-1991

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Frommer, William S.

/ REGISTRATION NUMBER: 25,506

/ REFERENCE/DOCKET NUMBER: 454310-2860

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (212) 840-3333

/ TELEFAX: (212) 840-0712

/ INFORMATION FOR SEQ ID NO: 130:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 1008 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA

/ US-09-354-138-130

/ Alignment Scores:

/ Pred. No.: 0.026

/ Score: 83.50

/ Percent Similarity: 46.30%

/ Best Local Similarity: 28.70%

/ Query Match: 12.03%

/ DB: 4 Gaps: 6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-354-138-130 (1-1008)

QY 2 LeuGlnLeuGluThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLys 21

DB 200 CTCATTTGGAAGAAATTTGATGCGCTGCTTGGAGTTGGGATCTACAGCCAGAC 259

QY 22 TrpGlnMetAlaSerSerGluProCysValAsnLysValSerAspTrp----- 38

DB 260 CTGAGGAGTTATTGAAGAAGCCACCCTGT-----TGATATTATGG 301

QY 39 -----LysLeuGluIleLeuGlnAsnGlyLeuTyLeuIleTyGlyGlnValAlaPro 56

DB 302 TAAGGGAATGAGAGTGTCAAGAACTGTATTATAT-----ATACACCC 352

QY 57 Asn-AlaAsnTyAsnAspVal-----AlaProPheGluValArgLeuTyLYeAsnLys 74

DB 353 CATTCACATCTTAATCTCCGTGAAAGAGTCTTACGAGTGAAGTGTTCAGTGCAA 412

QY 74 AspMetIle-----GlnThrLeuThrAsnLysSerLysIleGlnAsnVal 89

DB 413 ATCAAGTCTGTAACACAGTCATCTATATCCATTAGACATACCAAGATTACG----- 467

QY 89 LgiGlyThrTyGluLeuHis 96

DB 468 -GGTGGTATATAGACATCAC 488

RESULT 6

US-08-496-944-1

/ Sequence 1, Application US/08496944

/ Patent No. 6040496

/ GENERAL INFORMATION:

/ APPLICANT: Law, Marcus D

/ APPLICANT: Dietz, Jon M.

/ TITLE OF INVENTION: Use of translationally altered RNA to

/ TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other

/ NUMBER OF SEQUENCES: 8

/ CORRESPONDENCE ADDRESS:

/

/

/

/

/

/

/

/

ADDRESSEE: CIBA-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.308
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,944
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1814
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8543 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..8291
OTHER INFORMATION: /product= "polypeptide encoded by
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 8292..8530
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 3..1133
OTHER INFORMATION: /product= "3-prime sequence for
OTHER INFORMATION: HC-Pro"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 1134..2375
OTHER INFORMATION: /product= "P3 proteinase"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 2376..4292
OTHER INFORMATION: /product= "cylindrical inclusion
OTHER INFORMATION: Protein"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 4293..4451
OTHER INFORMATION: /product= "K2 (6kD protein)"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 4452..5744
OTHER INFORMATION: /product= "N1a proteinase"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 5745..7307
OTHER INFORMATION: /product= "N1b replicase"
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 7308..8291
OTHER INFORMATION: /product= "coat protein"
US-08-496-944-1
Alignment Scores:
Pred. No.: 6.75 Length: 8543
Score: 77.00 Matches: 20
Percent Similarity: 41.13% Conservative: 31
Best Local Similarity: 25.00% Mismatches: 53
Query Match: 11.10% Indels: 20

DB: 3 Gaps: 5
US-09-195-368-1_COPY_48_177 (1-130) x US-08-496-944-1 (1-8543)
QY 4 LeuGluThrAlaLeuGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGln 23
DB 54 AUCACAUUUUAUCAAAGAAAGGUGCAUCCAAUUUUUGCAUUUUAUCCACCAUUGGCAA 113
QY 24 MetAlaSerSerGluProCysValAsnLysValSerAspTrpLysLeuGluLeu 43
DB 114 GUGCGGAACAAUAGGCGCAUUAUAGCAUUAACCAAGUAAAGCAAAUUAUGAUGUU--- 170
QY 44 GluAsnGlyLeuTrpLeuIleTrpGlnValAlaProAsnAlaSerTrpAsnAspVal 63
DB 171 AGCGAAGCGCUCUACAAAGUUAUACUCCUAGUUGUUGCUAUGAAGCAAGCAAGCCCA 230
QY 64 AlaProPheGluVal---ArgLeuTrpLysAsnLys-----AspMet 76
DB 231 GCGUUAUUAUAGUUGCGCAUUGUUAUAGUUAUAGUUAUAGUUAUAGUUAUAGUUAU 290
QY 77 IlegInThrLeuThrAsnLysSerLysIleGlnMetValGlyGlyThrTrpGluLeuHis 96
DB 291 UUGGAUUCUUUAGAAUAAA-----AUACA 317
QY 97 ValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsn---Asn 115
DB 318 CCAAAGAGUACAUAAUAGCAUUAUAGUUGCGCAUUAUAGUUAUAGUUAUAGUUAU 377
QY 116 ThrTrpTrpGly 119
DB 378 UUUUAUUGGGGU 389
RESULT 7
US-08-998-416-717/C
/ Sequence 717, Application US/08998416
/ Patent No. 6239264
/ GENERAL INFORMATION:
/ APPLICANT: Philippson, Peter
/ APPLICANT: Pohlmann, Rainer
/ APPLICANT: Steiner, Sabine
/ APPLICANT: Mohr, Christine
/ APPLICANT: Wendland, Ulfgen
/ APPLICANT: Knechtle, Philipp
/ APPLICANT: Reibischung, Corinne
/ TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
/ NUMBER OF SEQUENCES: 1152
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 6239264artis Corporation
/ STREET: 3054 Cortwallis Road
/ CITY: Research Triangle Park
/ STATE: No. 6239264th Carolina
/ COUNTRY: USA
/ ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689

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? INFORMATION FOR SEQ ID NO: 717
? SEQUENCE CHARACTERISTICS:
? LENGTH: 699 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? ORIGINAL SOURCE:
? ORGANISM: PGL1470RP
?
US-08-998-416-717

```

Pred. No.:	0.303	length:	699
Score:	74.50	Matches:	37
Percent Similarity:	40.60%	Conservative:	17
Best Local Similarity:	27.82%	Mismatches:	60
Query Match:	10.73%	Indels:	19
DB:	3	Gaps:	6

US-09-195-368-1_COPY_48_177 (1-130) X US-08-998-416-717 (1-699)

```

Oy      GlnLeuGlnIunhPhrAlaLysGluProCysMetalAlaLysPheGlyPro-----LeuProSer 20
Db      444  GAGCTTGAAGACTGAGCTCGCGCGGATGAAGAGCGAGATGTCACCGCACTGTTATCAG 385
Oy      21  LysTrpGlnMetalaseSerGluProCysValAsnLysValSerAspTrpLysLeu 40
Db      384  AAGACAGCTTATGGGCACAGCTGTCGCCCC-----GTGAACAGACTTTCGACAGTCACTT 333
Oy      41  GluLeuGlnIunhGlyLeuTrpLeuLeuIleTyrGlyGlnValAlaPheAsnAlaAsnTyr 60
Db      330  GTGATTAAGAGACGAGCGCCGACAGATCTTCACGGCGCAGCTTCATTTCGACGCGTCGC 271
Oy      61  AsnAspValAlaProPheGluValArgLeuTrpLysAsnLysAspMetIleGlnThrLeu 80
Db      270  GATTCTGTGAGTCCG-----CGGCTTCACATTATTTACTGTAATCTGACAGAG 222
Oy      81  ThrAsnLys-----SerLysIleGlnAsnValGlyThrTyrGluLeu 95
Db      219  TTGGCGCATGCGCTGCTCTTGGAAGAAAGATTAATTACTACTCGCGATGTGAGCTA 160
Oy      96  HisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsn 115
Db      159  -----GATTTGATGAGACACACTTCATGACGGAACAGAA-----CAG 121
Oy      116  ThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPhe 128
Db      120  AACCTACTGGGGGGGCTTTCGTGCTGCGCTTCCTTCGAGACTAT 82

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RESULT 8
5182196-3
PATENT NO. 5182196
APPLICANT: ALLET, BERNARD; KAWASHIMA, ERIC H.
TITLE OF INVENTION: EXPRESSION SYSTEMS FOR OVERPRODUCTION OF
DESIRED PROTEINS
NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/372,281
FILING DATE: 27-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 53,398
FILING DATE: 18-MAY-1987
APPLICATION NUMBER: 785,847
FILING DATE: 09-OCT-1985
SEQ ID NO:3:
LENGTH: 935
5182196-3

Alignment Scores:	
Pred. No.:	0.568
Score:	74.00
Percent Similarity:	39.01%
Best Local Similarity:	26.24%
Length:	93
Matches:	37
Conservative:	18
Mismatches:	38

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Query Match: 10.66% Indels: 45
DB: 6 Gaps: 8
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US-09-195-368-1_COPY_48_177 (1-130) X 5182196-3 (1-935)

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Oy      16  G|A|P|L|E|U|P|S|E|R|E|T|P|G|I|M|E|R|A|L|S|E|R|S|E|R|I|N|P|R|O|C|Y|S|V|A|L|E|N|T|S|V|A|L 35
Db      510  GGGCCCAATGCTCTCC---TGCCCAATGCGCTG-----GAGCTG 544
Oy      36  S|e|r|A|s|P|T|P|L|y|S|e|u|G|h|u|I|e|u|G|I|n|a|n|g|I|e|u|T|y|I|e|u|I|e|T|y|G|I|y|G|I|N|V|A|--- 54
Db      545  A|G|A|T|A|A|C|C|A|G|C|T|G|T|G|T|G|T|G|C|A|T|C|A|A|G|G|C|C|T|G|T|A|C|C|T|A|C|T|C|T|C|C|A|G|G|T|C|T|C 604
Oy      55  -----A|A|P|r|o|s|n|A|a|n|T|y|r-----A|s|n|A|P|V|A|I|A|P|r|O|P|h|e 66
Db      605  T|T|C|A|A|G|G|G|C|C|A|A|G|G|T|G|C|C|C|C|T|T|C|A|C|C|A|T|G|N|C|T|C|T|C|A|C|C|C|A|C|A|C|A|T|C|A|G|G|C|G|A|T|C 664
Oy      67  G|U|V|A|I|A|S|E|U|T|Y|I|D|Y|S|A|N|T|Y|S|A|S|P|E|T|I|E|G|I|N|T|H|I|E|U|T|H|R|A|S|E|U|T|Y|S|E|R|Y|S|E|I|E 86
Db      665  G|C|G|C|T|C|C|T|C|C|A|C|A|G|A|C|C|A|A|G|T|C|A|A|C|C|T|C|T|C|T|G|C|A|T|C---A|A|G|A|G|C|C|C|T|G|C 718
Oy      87  G|I|A|n|s|-----V|A|I|G|I|y 90
Db      719  C|A|G|A|G|G|A|G|A|C|C|C|C|A|G|G|G|G|G|G|T|A|G|G|C|C|A|A|C|C|C|T|G|T|A|T|G|A|G|C|C|A|T|A|T|A|C|T|T|G|G|A 778
Oy      91  G|I|T|H|T|Y|G|I|U|D|E|U|H|I|S|V|A|I|G|I|A|S|P|T|H|I|E|A|P----- 102
Db      779  G|G|G|G|T|C|T|T|C|A|G|T|G|A|A|G|G|G|T|A|C|C|A|C|G|T|C|A|C|G|C|T|A|G|A|T|C|A|T|C|G|G|C|C|G|C|A|T|T 838
Oy      103  L|e|u|I|e|P|h|e|A|n|S|E|R|G|I|N|H|I|S|G|I|N|V|A|L|E|U|T|Y|S|A|S|A|N|A|N|T|H|T|Y|T|P|G|I|Y|I|E|I|L|E|U 122
Db      839  C|T|G|A|C|T|T|T|C|C|C|A|G|T|C|G|G|C|A|G|G|T|C-----T|A|C|T|T|G|G|G|A|T|C|A|T|T|G|C 883
Oy      123  L|e|u 123
Db      884  C|T|G 886

```

RESULT 9
 US-08-697-610-1
 ; Sequence 1, Application US/08697610
 ; Patent No. 6172187
 ;
 GENERAL INFORMATION:
 ;
 APPLICANT: Reed, John C.
 APPLICANT: Sato, Takaki
 TITLE OF INVENTION: CD40 Associated Proteins
 NUMBER OF SEQUENCES: 17
 ;
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 7000
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ;
 ZIP: 92122
 ;
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 ;
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/697,610
 FILING DATE:
 CLASSIFICATION: 530
 ;
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/349,357
 FILING DATE: 02-DEC-1994
 ;
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LJ 1203
 ;
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 ;
 INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 137..1766
US-08-697-610-1

Alignment Scores:
Pred. No.: 2.25 Length: 2240
Score: 74.00 Matches: 28
Percent Similarity: 45.45% Conservative: 17
Best Local Similarity: 28.28% Mismatches: 24
Query Match: 10.66% Indels: 30
Gaps: 6
DB: 3

US-09-195-368-1_COPY_48_177 (1-130) x US-08-697-610-1 (1-2240)

QY 25 AlaSerSerGluProProCysValAlaSerAspTTP----- 38
DB 818 GCCAGCTCCGCCGTGCACAGCAGCTCACTGAAAGAGTGAACAACCTCGTCAAAAG 877
QY 39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58
DB 878 AAGCTTCCTTGTGAGAAAT-----GAAAGTGAAGAAAAAACAAG 919
QY 59 Asn-----TyrAsnAspValAlaProPheGlnValArgLeuTyrLysAsnLys 74
DB 920 AGCATACAAAGTTTGCAATCAGATATAGCTTTGAATTTGAATTTGACACAAAG 979
QY 75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGln 94
DB 980 GAAATGCTTGA-----AATATGATCAATCAAAATC----- 1009
QY 95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGlnHisGlnValLeuLys 113
DB 1010 CTTCAATTACAGCAGAGTGATAGAC-----AGCCAAGCAGAGAACTGAAG 1054

RESULT 10
US-08-349-357-1
Sequence 1, Application US/08349357
Patent No. 6265556
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: CD40 Associated Proteins
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/349,357
FILING DATE: 02-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1203
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 2240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 137..1766
US-08-349-357-1

Alignment Scores:
Pred. No.: 2.25 Length: 2240
Score: 74.00 Matches: 28
Percent Similarity: 45.45% Conservative: 17
Best Local Similarity: 28.28% Mismatches: 24
Query Match: 10.66% Indels: 30
Gaps: 6
DB: 3

US-09-195-368-1_COPY_48_177 (1-130) x US-08-349-357-1 (1-2240)

QY 25 AlaSerSerGluProProCysValAlaSerAspTTP----- 38
DB 818 GCCAGCTCCGCCGTGCACAGCAGCTCACTGAAAGAGTGAACAACCTCGTCAAAAG 877
QY 39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAla 58
DB 878 AAGCTTCCTTGTGAGAAAT-----GAAAGTGAAGAAAAAACAAG 919
QY 59 Asn-----TyrAsnAspValAlaProPheGlnValArgLeuTyrLysAsnLys 74
DB 920 AGCATACAAAGTTTGCAATCAGATATAGCTTTGAATTTGAATTTGACACAAAG 979
QY 75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGln 94
DB 980 GAAATGCTTGA-----AATATGATCAATCAAAATC----- 1009
QY 95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGlnHisGlnValLeuLys 113
DB 1010 CTTCAATTACAGCAGAGTGATAGAC-----AGCCAAGCAGAGAACTGAAG 1054

RESULT 11
US-09-645-926A-6
Sequence 6, Application US/09645926A
Patent No. 6482411
GENERAL INFORMATION:
APPLICANT: AHUJA, SEEMA
APPLICANT: BONEWALD, LYNDIA
TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4003,001000
CURRENT APPLICATION NUMBER: US/09/645,926A
CURRENT FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/151,250
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 2339
TYPE: DNA
ORGANISM: Homo sapiens
US-09-645-926A-6

Alignment Scores:
Pred. No.: 2.41 Length: 2339
Score: 74.00 Matches: 28
Percent Similarity: 45.45% Conservative: 17
Best Local Similarity: 28.28% Mismatches: 24
Query Match: 10.66% Indels: 30
Gaps: 6
DB: 4

US-09-195-368-1_COPY_48_177 (1-130) x US-09-645-926A-6 (1-2339)

QY 25 AlaSerSerGluProProCysValAlaSerAspTTP----- 38

Db 964 GCCAGCTCCGCCGTCGACGACCTGCTGAAGAGTGGAGCAACTCGTCAAAAG 1023
QY 39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAspAla 58
Db 1024 AAGGTTTCCTGTTGCGAAT-----GAAAGTGTGAAAAAACAAG 1065
QY 59 Asn-----TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74
Db 1066 AGCATACAAAGTTTGCAACATCAGATATGAGCTTGAATGAAATTGAGACAAAAAG 1125
QY 75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94
Db 1126 GAAATGCTTCGA-----AATATGAAATCCAAATC----- 1155
QY 95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113
Db 1156 CTTCATTTACAGCAGCATGATGAC-----AGCCACAGCAGAAACTGGAAG 1200

RESULT 12
PCT-US95-16980-1
Sequence 1, Application PC/TUS9516980
GENERAL INFORMATION:
APPLICANT: Brigham & Women's Hospital
TITLE OF INVENTION: CONTROLLING TRAF-MEDIATED SIGNALS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16980
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/367,540
FILING DATE: 30-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 05311/014K01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEFAX: (617)542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2359 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 151..1854
PCT-US95-16980-1

Alignment Scores:
Pred. No.: 2.44 Length: 2359
Score: 74.00 Matches: 28
Percent Similarity: 45.45% Conservative: 17
Best Local Similarity: 28.28% Mismatches: 24
Query Match: 10.66% Indels: 30
Gaps: 6

US-09-195-368-1_COPY_48_177 (1-130) x PCT-US95-16980-1 (1-2359)

QY 25 AlaSerSerGluProProCysValAsnLysValSerAspTyr----- 38
Db 907 GCCAGCTCCGCCGTCGACGACCTGCTGAAGAGTGGACCACTGCTCGAAAAG 966
QY 39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAspAla 58
Db 967 AAGGTTTCCTGTTGCGAAT-----GAAAGTGTGAAAAAACAAG 1008
QY 59 Asn-----TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74
Db 1009 AGCATACAAAGTTTGCAACATCAGATATGAGCTTGAATGAAATTGAGACAAAAAG 1068
QY 75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94
Db 1069 GAAATGCTTCGA-----AATATGAAATCCAAATC----- 1098
QY 95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113
Db 1099 CTTCATTTACAGCAGCATGATGAC-----AGCCACAGCAGAAACTGGAAG 1143

RESULT 13
US-09-167-109-3
Sequence 3, Application US/09167109
Patent No. 639297
GENERAL INFORMATION:
APPLICANT: Baker, Brenda F.
APPLICANT: Cowser, Lex M.
APPLICANT: Monta, Bret P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/09/167,109
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
SEQ ID NO 3
LENGTH: 2455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (218)..(1924)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: U21092
DATABASE ENTRY DATE: 1995-03-23
US-09-167-109-3

Alignment Scores:
Pred. No.: 2.6 Length: 2455
Score: 74.00 Matches: 28
Percent Similarity: 45.45% Conservative: 17
Best Local Similarity: 28.28% Mismatches: 24
Query Match: 10.66% Indels: 30
Gaps: 6

US-09-195-368-1_COPY_48_177 (1-130) x US-09-167-109-3 (1-2455)

QY 25 AlaSerSerGluProProCysValAsnLysValSerAspTyr----- 38
Db 974 GCCAGCTCCGCCGTCGACGACCTGCTGAAGAGTGGACCACTGCTCGAAAAG 1033
QY 39 LysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAspAla 58
Db 1034 AAGGTTTCCTGTTGCGAAT-----GAAAGTGTGAAAAAACAAG 1075
QY 59 Asn-----TyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLys 74
Db 1076 AGCATACAAAGTTTGCAACATCAGATATGAGCTTGAATGAAATTGAGACAAAAAG 1135
QY 75 AspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGlu 94
Db 1136 GAAATGCTTCGA-----AATATGAAATCCAAATC----- 1165
QY 95 LeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 113

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Db      1166 CTTCAATTACAGGAGTATCGAC-----AGCCACAGAGAAATGTAAG 1210
|||||
RESULT 14
US-09-540-236-384/c
; Sequence 384, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 384
; LENGTH: 2925
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-384

Alignment Scores:
Pred. No.:      3.43      Length:      2925
Score:          74.00     Matches:      31
Percent Similarity: 39.23% Conservative: 20
Best Local Similarity: 23.85% Mismatches: 52
Query Match:     10.66% Indels:      27
                        Gaps:        6
DB:                4

US-09-195-368-1_COPY_48_177 (1-130) x US-09-540-236-384 (1-2925)
Qy      14 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysVal--- 32
      |||
Db      451 AAGCTGCACCAATAAATCGCTGCGAGATTTTCAACATTCAAAACCGTGGCTTGA 392
      |||
Qy      33 -----AsnLysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrlleuile 50
      |||
Db      391 CTGTTTCAGGCAATGAACTCATGGCAGATTTGTAATTTAT-----TTTGACTTGTGA 341
      |||
Qy      51 TyrlGlnIValAlaProAsnAlaAsnTyrlAsnAspValAlaProPheGlnValArgLeu 70
      |||
Db      340 CTTGGGCGG-----TATCTGATCAGTCCATTTCAA-----ATG 305
      |||
Qy      71 TyrlAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGly 90
      |||
Db      304 TTAAGTCACAGAGCAGACCCCTCCGCTGATGAAATTGATGACATGATCATCATCAT 245
      |||
Qy      91 -GlyThrTyrlGlnLeuHisValGlyAspThrIleAspLeuIlePheAsn----- 106
      |||
Db      244 CAATCCCTTCATCTGCTGCTGATGATCGCGTACCGAGTTTTCACACCGCTCAGCAT 185
      |||
Qy      107 -----SerGlnHisGlnValLeuLysAsnAsnThrTyrlTrpGlyIleI 121
      |||
Db      184 CAGCACTGGGTAAAGCAGCAGCCTTACTTACGCGGTGCAATTTTGG----- 133
      |||
Qy      121 eleuLeuAlaAsnProGlnPheIleSer 130
      |||
Db      132 -GTATTGTTCAATCGCAAAATTATTAAT 106
      |||

RESULT 15
US-09-536-002-37/c
; Sequence 37, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
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; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 37
; LENGTH: 99629
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 78467
; OTHER INFORMATION: a or g or c or t, unknown, or other
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte template ID No. 6632636 37
; PUBLICATION INFORMATION:
US-09-536-002-37

Alignment Scores:
Pred. No.:      889      Length:      99629
Score:          74.00     Matches:      31
Percent Similarity: 39.23% Conservative: 20
Best Local Similarity: 23.85% Mismatches: 52
Query Match:     10.66% Indels:      27
                        Gaps:        6
DB:                4

US-09-195-368-1_COPY_48_177 (1-130) x US-09-536-002-37 (1-99629)
Qy      14 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysVal--- 32
      |||
Db      3115 AAGCTGCACCAATAAATCGCTGCGAGATTTTCAACATTCAAAACCGTGGCTTGA 3056
      |||
Qy      33 -----AsnLysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrlleuile 50
      |||
Db      3055 CTGTTTCAGGCAATGAACTCATGGCAGATTTGTAATTTAT-----TTTGACTTGTGA 3005
      |||
Qy      51 TyrlGlnIValAlaProAsnAlaAsnTyrlAsnAspValAlaProPheGlnValArgLeu 70
      |||
Db      3004 CTTGGGCGG-----TATCTGATCAGTCCATTTCAA-----ATG 2965
      |||
Qy      71 TyrlAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGly 90
      |||
Db      2966 TTAAGTCACAGAGCAGACCCCTCCGCTGATGAAATTGATGACATGATCATCATCAT 2909
      |||
Qy      91 -GlyThrTyrlGlnLeuHisValGlyAspThrIleAspLeuIlePheAsn----- 106
      |||
Db      2908 CAATCCCTTCATCTGCTGCTGATGATCGCGTACCGAGTTTTCACACCGCTCAGCAT 2849
      |||
Qy      107 -----SerGlnHisGlnValLeuLysAsnAsnThrTyrlTrpGlyIleI 121
      |||
Db      2848 CAGCACTGGGTAAAGCAGCAGCCTTACTTACGCGGTGCAATTTTGG----- 2797
      |||
Qy      121 eleuLeuAlaAsnProGlnPheIleSer 130
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Db      2796 -GTATTGTTCAATCGCAAAATTATTAAT 2770
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Search completed: April 7, 2004, 21:12:32
Job time : 76.9316 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 18:25:49 ; Search time 204.104 Seconds
(without alignments)
2387.053 Million cell updates/sec

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Perfect score: 694
Sequence: 1 FLOLETAKEPCAKFGPLPS.....VLKNTYGCITLILANPDIS 130

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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2470632 segs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-LOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09195368 @CGN.1.1.409 @runat_07042004_061640_2686
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Database: Published Applications NA:*

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2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
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11: /cgn2_6/prodata/1/pubpna/us09_NEW_PUB.seq:*
12: /cgn2_6/prodata/1/pubpna/us10A_PUBCOMB.seq:*
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14: /cgn2_6/prodata/1/pubpna/us10C_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/us10_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match Length	ID	Description
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1	694	100.0	534	12	US-10-202-062-39	Sequence 39, Appl
2	694	100.0	534	14	US-10-272-411-9	Sequence 9, Appl
3	694	100.0	534	14	US-10-218-547-39	Sequence 39, Appl
4	694	100.0	534	14	US-10-272-328A-9	Sequence 9, Appl
5	694	100.0	534	14	US-10-110-793-43	Sequence 43, Appl
6	694	100.0	1849	9	US-09-345-790-1	Sequence 1, Appl
7	694	100.0	1849	13	US-10-136-511-1	Sequence 1, Appl
8	694	100.0	1964	13	US-10-080-485-2	Sequence 2, Appl
9	694	100.0	1964	13	US-10-116-378-27	Sequence 15, Appl
10	694	100.0	1964	13	US-10-116-378-27	Sequence 15, Appl
11	107	15.4	60	15	US-09-908-975-14130	Sequence 14130, A
12	92	13.3	1008	10	US-10-131-827-2732	Sequence 2732, Ap
13	83.5	12.0	1008	10	US-09-951-061A-110	Sequence 130, Ap
14	80	11.5	3275	12	US-10-205-331-15	Sequence 15, Appl
15	80	11.5	3275	15	US-10-388-934-37	Sequence 37, Appl
16	78	11.2	474	14	US-10-297-942-1	Sequence 1, Appl
17	76	11.0	449	10	US-09-918-995-2646	Sequence 2646, Ap
18	75.5	10.9	17388	9	US-09-815-242-8512	Sequence 8512, Ap
19	75	10.8	474	14	US-10-297-942-5	Sequence 5, Appl
20	74.5	10.7	9524	16	US-10-311-455-812	Sequence 812, Ap
21	74.5	10.7	9524	16	US-10-257-165-76	Sequence 76, Appl
22	74.5	10.7	13635	12	US-10-210-175-13	Sequence 13, Appl
23	74.5	10.7	13635	16	US-10-664-368-30	Sequence 30, Appl
24	74.5	10.7	14889	14	US-10-101-510-356	Sequence 356, App
25	74.5	10.7	14896	15	US-10-159-563-206	Sequence 206, App
26	74	10.7	474	14	US-10-297-942-3	Sequence 3, Appl
27	74	10.7	2240	9	US-09-757-041-1	Sequence 1, Appl
28	74	10.7	2339	14	US-10-242-212-6	Sequence 6, Appl
29	74	10.7	2339	14	US-10-207-655-102	Sequence 102, App
30	74	10.7	2359	8	US-08-813-333A-3	Sequence 3, Appl
31	74	10.7	2455	8	US-08-813-333A-4	Sequence 4, Appl
32	74	10.7	2455	14	US-10-067-125-3	Sequence 3, Appl
33	74	10.7	3153	12	US-10-282-122A-26786	Sequence 26786, A
34	74	10.7	4217	15	US-10-369-493-2731	Sequence 2731, A
35	73	10.5	499	12	US-10-085-783A-56227	Sequence 56227, A
36	73	10.5	499	15	US-10-242-535A-56227	Sequence 56227, A
37	73	10.5	1545	14	US-10-295-074A-48	Sequence 48, Appl
38	73	10.5	1545	14	US-10-295-074A-50	Sequence 50, Appl
39	73	10.5	1545	14	US-10-295-074A-58	Sequence 58, Appl
40	73	10.5	1554	14	US-10-295-074A-52	Sequence 52, Appl
41	72	10.4	345	12	US-10-424-599-87615	Sequence 87615, A
42	72	10.4	477	14	US-10-295-074A-16	Sequence 16, Appl
43	72	10.4	1203	10	US-09-822-846-567	Sequence 567, App
44	72	10.4	1277	12	US-10-425-114-1431	Sequence 1431, Ap
45	72	10.4	1410	12	US-10-424-599-106051	Sequence 106051,

ALIGNMENTS

RESULT 1
US-10-202-062-39
; Sequence 39, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PFS59
; CURRENT APPLICATION NUMBER: US/10/202,062
; PRIOR APPLICATION NUMBER: 2002-07-25
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 534
; TYPE: DNA
; ORGANISM: human
US-10-202-062-39

Alignment Scores:

Pred. No.:	3.9e-90	Length:	534
Score:	694.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0

Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) X US-10-136-511-1 (1-1849)

QY 1 PheLeuGlnLeuGlnThrAlaValGluProCysMetAlaValPheGlyProLeuProSer 20
DB 170 TTTCTCCAAATTAGAGCTGCTAAGAGCCCTGTAAGCTTAAGTTGGACCATTAACCTCA 229
QY 21 LysTrpGlnMetAlaSerSerGluProCysValAsnLysValSerAspTrpLysLeu 40
DB 230 AAATGCCAAATGGCACTCTTGAACTCTTCGCGTAAATAGAGTGTCTGACGAAAGCTG 289
QY 41 GluLeuGlnAsnGlyLeuTyrluLeuIleTyrglyGlnValAlaProAsnAlaAsnTy 60
DB 290 GAGATCTTCAGAAATGGCTTAATTTAATTTATGGCAAGTGGCTCCCAATGCCAAACTAC 349
QY 61 AsnAspValAlaProPheGluValArgLeuTyrlsAsnLysAspMetIleGlnThrLeu 80
DB 350 AATGATGATGCTCTTTTGAAGTGGCGCTGTATATAAACAAGACATGATACAACTCTA 409
QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrglyLeuHisValGlyAspThr 100
DB 410 ACAAAACAATCTAAATCCAAATGTAGAGGAGCACTTAATGATTCATGTTGGGACACC 469
QY 101 IleAspLeuIlePheAsnSerGluHisGlnValIleLysAsnThrTyrlTrpGlyIle 120
DB 470 ATGACTGTGATTTCACTGACCTGAGCATCGATTCTTAATAAATATATCACTGAGGATATC 529
QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
DB 530 ATTTTACTAGCAAAATCCCAATTCATCTCC 559

RESULT 8

US-10-080-455-2
Sequence 2, Application US/10080455
Publication No. US20020146389A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Mark, Melanie R.
APPLICANT: Marsters, Scot A.
APPLICANT: Pitti, Robert M.
TITLE OF INVENTION: DAI19355 Polypeptide, A Tumor Necrosis Factor Homolog
FILE REFERENCE: P1150R2
CURRENT APPLICATION NUMBER: US/10/080,455
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/195,368
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: US 60/069,661
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: US 60/065,635
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 1964
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 1857, 1875
OTHER INFORMATION: n may be any nucleotide
US-10-080-455-2

Alignment Scores:
Pred. No.: 2,98e-89 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) X US-10-080-455-2 (1-1964)

QY 1 PheLeuGlnLeuGlnThrAlaValGluProCysMetAlaValPheGlyProLeuProSer 20
DB 162 TTTCTCCAAATTAGAGCTGCTAAGAGCCCTGTAAGCTTAAGTTGGACCATTAACCTCA 221
QY 21 LysTrpGlnMetAlaSerSerGluProCysValAsnLysValSerAspTrpLysLeu 40
DB 222 AAATGCCAAATGGCACTCTTGAACTCTTCGCGTAAATAGAGTGTCTGACGAAAGCTG 281
QY 41 GluLeuGlnAsnGlyLeuTyrluLeuIleTyrglyGlnValAlaProAsnAlaAsnTy 60
DB 282 GAGATCTTCAGAAATGGCTTAATTTAATTTATGGCAAGTGGCTCCCAATGCCAAACTAC 341
QY 61 AsnAspValAlaProPheGluValArgLeuTyrlsAsnLysAspMetIleGlnThrLeu 80
DB 342 AATGATGATGCTCTTTTGAAGTGGCGCTGTATATAAACAAGACATGATACAAACTCTA 401
QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrglyLeuHisValGlyAspThr 100
DB 402 ACAAAACAATCTAAATCCAAATGTAGAGGAGCACTTAATGATTCATGTTGGGACACC 461
QY 101 IleAspLeuIlePheAsnSerGluHisGlnValIleLysAsnThrTyrlTrpGlyIle 120
DB 462 ATGACTGTGATTTCACTGACCTGAGCATCGATTCTTAATAAATATATCACTGAGGATATC 521
QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
DB 522 ATTTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 9

US-10-116-378-15
Sequence 15, Application US/10116378
Publication No. US20020150993A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Marsters, Scot A.
APPLICANT: Pitti, Robert M.
APPLICANT: Wood, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
PRIOR FILING DATE: EARLIER FILING DATE: 1995-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 15
LENGTH: 1964
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 1857, 1875
OTHER INFORMATION: n may be any nucleotide
US-10-116-378-15

Alignment Scores:
Pred. No.: 2,98e-89 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-116-378-15 (1-1964)

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QY 1 PheleuglnleugluthThAlaIySGluProCySmetAlaIySPheGlyProLeuProSer 20
DB 162 TTTCTCCATTAGAGACTGCTTAAGAGAGCCCTGTATGGCTTAAGTTTGAACATTACCTCA 221
QY 21 LysTPGlnMeAlaSerSerglUProProCySValAsnlySValSerAspTIPlySLeu 40
DB 222 AAATGGCAATGGACATCTTCTGAACCTCTGCGTGAATAGAGTGTGACTGGAACTG 281
QY 41 GluIleleuglnAsnGlyLeuTyIleuIleTyIleGlyGlnValAlaProAsnAlaAsnTyI 60
DB 282 GAGAACTTCAGAAAGGCTTATATTATTAATGCGCAAGGCTCCCAATGCAAACTAC 341
QY 61 AsnAspValAlaProPheGluValArgLeuTyIleAsnlySAspMetIleGlnThLeu 80
DB 342 AATGATGTAGCTCTCTTTGAGGTGGGCTGTATAAAACAAAGACATGATCAAACTCA 401
QY 81 ThrAsnlySserIleGlnAsnValGlyGlyThTyIleuHsValGlyAspThr 100
DB 402 ACAACCAATCTAAATCTCAAAATGTAAGAGGACTTATGATTCATGTTGGGGACACC 461
QY 101 IleAspLeuIlePheAsnSerglUHiGlnValIleuIleAsnAsnThTyIleGlyIle 120
DB 462 ATAGACTTGATTTTCACTCTGAGCATGAGTTCTTAAAAATATATACATCTGGGGTATC 521
QY 121 IleleuIleuAlaAsnProGlnPheIleSer 130
DB 522 ATTTACTAGCAAAATCCCAATTCATCTCC 551
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RESULT 10

US-10-116-378-27/C
; Sequence 27, Application US/10116378
; Publication No. US2002015093A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pitei, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 27
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: 90, 108
; OTHER INFORMATION: n may be any nucleotide
US-10-116-378-27

Alignment Scores:

Pred. No.: 2,986-89 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x US-10-116-378-27 (1-1964)

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QY 1 PheleuglnleugluthThAlaIySGluProCySmetAlaIySPheGlyProLeuProSer 20
DB 1803 TTTCTCCATTAGAGACTGCTTAAGAGAGCCCTGTATGGCTTAAGTTTGAACATTACCTCA 1744
QY 21 LysTPGlnMeAlaSerSerglUProProCySValAsnlySValSerAspTIPlySLeu 40
DB 1743 AAATGGCAATGGACATCTTCTGAACCTCTGCGTGAATAGAGTGTGACTGGAACTG 1684
QY 41 GluIleleuglnAsnGlyLeuTyIleuIleTyIleGlyGlnValAlaProAsnAlaAsnTyI 60
DB 1683 GAGAACTTCAGAAAGGCTTATATTATTAATGCGCAAGGCTCCCAATGCAAACTAC 1624
QY 61 AsnAspValAlaProPheGluValArgLeuTyIleAsnlySAspMetIleGlnThLeu 80
DB 1623 AATGATGTAGCTCTCTTTGAGGTGGGCTGTATAAAACAAAGACATGATCAAACTCA 1564
QY 81 ThrAsnlySserIleGlnAsnValGlyGlyThTyIleuHsValGlyAspThr 100
DB 1563 ACAACCAATCTAAATCTCAAAATGTAAGAGGACTTATGATTCATGTTGGGGACACC 1504
QY 101 IleAspLeuIlePheAsnSerglUHiGlnValIleuIleAsnAsnThTyIleGlyIle 120
DB 1503 ATAGACTTGATTTTCACTCTGAGCATGAGTTCTTAAAAATATATACATCTGGGGTATC 1444
QY 121 IleleuIleuAlaAsnProGlnPheIleSer 130
DB 1443 ATTTACTAGCAAAATCCCAATTCATCTCC 1414
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RESULT 11

US-09-908-975-14130
; Sequence 14130, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, AVI
; APPLICANT: WASSERMAN, ALON
; APPLICANT: MINTZ, ELLI
; APPLICANT: MINTZ, LIAT
; APPLICANT: FAIGER, SIMCHON
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: Patentin version 3.10
; SEQ ID NO 14130
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-14130

Alignment Scores:

Pred. No.: 6,056-07 Length: 60
Score: 107.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.42% Indels: 0
DB: 10 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x US-09-908-975-14130 (1-60)

```
QY 25 AlaSerSerglUProProCySValAsnlySValSerAspTIPlySLeuGlnIleGln 44
DB 1 GCATCTTGAACCTCTTGGCTGATATAGAGTGTGACTGGAAGCTGGAAGTACTTCTAG 60
```

RESULT 12

US-10-131-827-2732
; Sequence 2732, Application US/10131827
; Publication No. US20040009479A1


```

RESULT 14
US-10-205-331-15
; Sequence 15, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alstair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WI-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 3275
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Cytosolic 3-hydroxy 3-methylglutaryl coenzyme A synthase
US-10-205-331-15

Alignment Scores:
Pred. No.: 2.46 Length: 3275
Score: 80.00 Matches: 28
Percent Similarity: 43.97% Conservative: 23
Best Local Similarity: 24.14% Mismatches: 39
Query Match: 11.53% Indels: 26
DB: Gaps: 5

US-09-195-368-1_COPY_48_177 (1-130) x US-10-205-331-15 (1-3275)

QY 20 SerlySTPGImetAlaSerSerglu-----ProProCysValAsnLys 34
DB 1458 TCAGAGTGATGAAAGCAGAGAAAGAACTTACGCCCGCGCTCCCAAAATGACACCA 1517
QY 35 Val-----SerAPTPLyLeuGluileuGlnasnGlyLeuTyrlleTyrgly 52
DB 1518 GTTGGATGAAGAGATGGGACTTG---TGCATTCAACACAGCTACAGACATA----- 1568
QY 53 GlnValAlaProAsnAlaAsnTyraAsnAspValAlaProPheGluValArgLeuTyrls 72
DB 1569 -----TTCCAAAGCCCGCTAAGAAAG 1589
QY 73 AsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThr 92
DB 1590 TGCCAAGACTTCTCGACCTCGGCGCGAAGCTGAGTGGCTGTCTCATCACTAAGCGGAGGC 1649
QY 93 TyrGlu-----LeuHisValGlyAspThrIleAspLeuIlePheAsnSergluHis 109
DB 1650 ACTGAGAGCCGCGCTTCACAGAGGCTCGGAGCTGATGGGTAATGGGAAACGTTAGAG 1709
QY 110 GlnValleuLysAsnAsnThrTyrrTpGlyIleIleLeuLeuAlaAsn 125
DB 1710 GAATGATGCTCTGGGACATTTTACAGATTACGTTGCTTAAAAAT 1757

RESULT 15
US-10-388-934-37
; Sequence 37, Application US/10388934
; Publication No. US20040005547A1
; GENERAL INFORMATION:
; APPLICANT: Boese, Franziska
; APPLICANT: Suter-Dick, Laura
; APPLICANT: Wolf, Detlef
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
; FILE REFERENCE: 21199
; CURRENT APPLICATION NUMBER: US/10/388,934
; CURRENT FILING DATE: 2003-03-14

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; PRIOR APPLICATION NUMBER: 02005336.9
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 02015657.6
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 862
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 3275
; TYPE: DNA
; ORGANISM: Rattus norvegicus (No. US20040005547Alway rat)
US-10-388-934-37

Alignment Scores:
Pred. No.: 2.46 Length: 3275
Score: 80.00 Matches: 28
Percent Similarity: 43.97% Conservative: 23
Best Local Similarity: 24.14% Mismatches: 39
Query Match: 11.53% Indels: 26
DB: Gaps: 5

US-09-195-368-1_COPY_48_177 (1-130) x US-10-388-934-37 (1-3275)

QY 20 SerlySTPGImetAlaSerSerglu-----ProProCysValAsnLys 34
DB 1458 TCAGAGTGATGAAAGCAGAGAAAGAACTTACGCCCGCGCTCCCAAAATGACACCA 1517
QY 35 Val-----SerAPTPLyLeuGluileuGlnasnGlyLeuTyrlleTyrgly 52
DB 1518 GTTGGATGAAGAGATGGGACTTG---TGCATTCAACACAGCTACAGACATA----- 1568
QY 53 GlnValAlaProAsnAlaAsnTyraAsnAspValAlaProPheGluValArgLeuTyrls 72
DB 1569 -----TTCCAAAGCCCGCTAAGAAAG 1589
QY 73 AsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThr 92
DB 1590 TGCCAAGACTTCTCGACCTCGGCGCGAAGCTGAGTGGCTGTCTCATCACTAAGCGGAGGC 1649
QY 93 TyrGlu-----LeuHisValGlyAspThrIleAspLeuIlePheAsnSergluHis 109
DB 1650 ACTGAGAGCCGCGCTTCACAGAGGCTCGGAGCTGATGGGTAATGGGAAACGTTAGAG 1709
QY 110 GlnValleuLysAsnAsnThrTyrrTpGlyIleIleLeuLeuAlaAsn 125
DB 1710 GAATGATGCTCTGGGACATTTTACAGATTACGTTGCTTAAAAAT 1757

```

Search completed: April 8, 2004, 04:20:31
Job time : 218.104 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:53:26 ; Search time 231.205 Seconds
(without alignments)
2388.639 Million cells updates/sec

Title: US-09-195-368-1_COPY_48_177
Perfect score: 694
Sequence: 1 FIOLETAKPCKAKFGPLPS.....VIAKNTYGTILLANPQFIS 130

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N-Geneseq.250an04-QFWT=Isatpg-SUFFIX=ring-MINMATCH=0.1-IOOCL=50
-LOOPEXT=0-UNITs=bits-START=1-END=-1-MATRIX=blonsum62-TRANS=human40.cdi
-LIST=45-DOCALLIGN=200-THR SCORES=pcr-THR MAX=100-THR MIN=0-ALIGN=15
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-NO MAP-ILABEQUERY-NEG-SCORES=0-WAIT-DSPBLOCK=100-LONGIOG
-DEV-TIMEOUT=120-MARN-TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6
-FGAPEXT=7-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database : N-Geneseq.250an04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match Length	DB ID	Description
1	694	100.0	534 7	ACC57580 Polynucle
2	694	100.0	534 9	ACC57909 Human GIT
3	694	100.0	534 9	Adc35221 Human CDN
4	694	100.0	1809 3	AAV19135 Human end
5	694	100.0	1849 3	AAZ74936 CDNA enco
6	694	100.0	1849 3	AAZ57314 Human end
7	694	100.0	1849 8	AdA11463 Human end
8	694	100.0	1849 9	AdC01857 Human CDN

9	694	100.0	1964 2	AAx59844
10	694	100.0	1964 2	AAx87726
11	694	100.0	1964 4	AAc85435
12	694	100.0	1964 4	AAf30051
13	694	100.0	1964 4	AAc97374
14	694	100.0	1964 4	AAc85945
15	694	100.0	1964 4	AAc90563
16	694	100.0	1964 6	ABK28562
17	566	81.6	1527 5	AAx90614
18	566	81.6	1527 5	AAx90614
19	107	15.4	60 6	ABN41382
20	92	13.3	50 6	ABN202741
21	86	12.4	320 6	ABN18154
22	84.5	12.2	3666 6	ABD90678
23	83.5	12.0	1008 6	AB198960
24	83.5	12.0	15690 6	ABK15038
25	83.5	12.0	15690 6	ABK15000
26	83.5	12.0	18826 6	ABK15039
27	80	11.5	3275 8	ACP25333
28	80	11.5	3275 9	ADb58295
29	80	11.5	3275 9	ADb58284
30	80	11.5	3977 2	AAQ87698
31	80	11.5	3977 2	AAQ87699
32	78.5	11.3	1797 6	ABN66564
33	78.5	11.3	110000 6	ABN71527_07
34	78	11.2	474 6	ABA94384
35	78	11.2	477 2	AAV68423
36	77.5	11.2	1018 3	AAA44544
37	77	11.1	505 1	AAK91642
38	77	11.1	694 3	AAK47600
39	77	11.1	3977 2	AAQ87696
40	77	11.1	8298 2	AAV18096
41	77	11.1	8543 2	AAV47072
42	76	11.0	449 8	ACH15434
43	76	11.0	462 2	AAQ03594
44	76	11.0	462 2	AAQ02033
45	76	11.0	3977 2	AAQ87697

ALIGNMENTS

RESULT 1	ACC57580	standard; DNA; 534 BP.
AC	ACC57580;	
DT	28-JUN-2003	(first entry)
XX	Polynucleotide encoding tumour necrosis factor superfamily member.	
KW	Human; RANKL; tumour necrosis factor; osteopathic; bone; gene; ds.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO2003033663-A2.	
PN	24-APR-2003.	
PD	15-OCT-2002; 2002WO-US033022.	
XX	15-OCT-2001; 2001US-0329393P.	
PR	15-OCT-2001; 2001US-0329393P.	
XX	(BARN-) BARNES-JEWISH HOSPITAL.	
PA	Lam J, Ross PF, Teitelbaum SL;	
PI	WPI, 2003-430346/40.	
DR	New RANKL mink comprising a core, and at least one external loop, useful	
XX	for enhancing processes of bone formation or inhibiting bone resorption,	
PT	thus providing treatments for disease or condition characterized by loss	
PT	of bone mass.	

XX PS Disclosure; Page 58; 78bp; English.

CC The present sequence is that of a polynucleotide encoding a non-RANKL member of the tumour necrosis factor (TNF) superfamily. The invention provides non-naturally-occurring proteins that contain one or more of the external surface loops of RANKL (see ABR42066-70) in combination with a heterologous protein core obtained from a non-RANKL member of the TNF superfamily. Also provided are polynucleotides encoding such proteins. The proteins bind to RANK, acting as mimics of RANKL. They can be used to enhance bone formation by either inhibiting bone resorption or inducing osteogenesis, thus providing treatment for diseases or conditions characterized by loss of bone mass.

CC Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

XX SQ

Alignment Scores:

Pred. No.:	3,01e-78	Length:	534
Score:	694.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-09-195-368-1_COPY_48_177 (1-130) x ACC57909 (1-534)

QY 1 PheleuglnleugluthrAlaIygluProCysMetAlaIySpheglProleuProser 20

DB 142 TTTCTCCATTAGAGACTGCTAAGAGCCCTGTATGCTTAAGTTGACCATTAACCTCA 201

QY 21 LysTrpGlnMetAlaSerSerGluProProCysValAsnIySerAspTrpIySleu 40

DB 202 AAATGGCAATAGGATCTTCTGAACCTCTTGCCTGATAGATGCTGAGGAGCTG 261

QY 41 GlulleuglnAsnglyLeuTyIleuIleTyIyGlnValAlaProAsnAlaAsnTy 60

DB 262 GAGATACCTTCAGATGCTTATATTATTTATGCGCAATGCTCCCAATGCAAACTAC 321

QY 61 AsnAspValAlaProPhegluValArgleuTyIyAsnIyAspMetIleGlnThrIleu 80

DB 322 AATGATGAGCTCTTTGAGTGGCTGTATTAACAAAGACATGATACCAACTCA 381

QY 81 ThrAsnIySerIyIleGlnAsnValIyGlyThyTyIyGlnIleuHisValIyAspThr 100

DB 382 ACAACCAATCTAATCAAAATGAGAGGAGGACTTATGATGCTGTTGGGAGACCC 441

QY 101 IleAspIleuIlePheAsnSerGlnHisGlnValIleuIyAsnAsnTyTyTrpGlyIle 120

DB 442 ATGACTTGATATTCACACTGAGCATCAGGTTCTAATAAATAATACATACCTGGGATTC 501

QY 121 IleleuIleuAlaAsnProGlnPheIleSer 130

DB 502 ATTACTAGCAATCCCAATTCATCTCC 531

RESULT 2

ACC57909 standard; CDNA; 534 BP.

XX AC ACC57909;

DT 11-AUG-2003 (first entry)

XX Human GITRL polynucleotide.

XX Human, GITRL; tumour necrosis factor; ligand; cytostatic;

XX Immunomodulator; osteopathic; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT 1..534

XX CDS /*tag= a

FT /product= "Human GITRL"

XX PN WO2003040307-A2.

XX PD 15-MAY-2003.

XX PR 25-JUL-2002; 2002WO-US023782.

XX PR 27-JUL-2001; 2001US-0307838P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Hilbert DH, Rosen CA;

XX DR WPI; 2003-430659/40.

XX DR P-PSDB; ABR42323.

XX PT New heteromultimeric complex having a first polypeptide member of the

XX PT tumor necrosis factor (TNF) ligand family, and a second different member

XX PT of TNF ligand family, useful for treating cancer, osteoporosis or an

XX PT autoimmune disease.

XX PS Disclosure; Page 382; 388bp; English.

XX CC The present sequence is that of a polynucleotide encoding human GITRL.

XX CC The invention relates to compositions comprising heterotrimeric complexes

XX CC of tumour necrosis factor (TNF) ligand family members, and their use in

XX CC the detection, prevention and treatment of disease. In preferred

XX CC embodiments, the heterotrimeric complex comprises full-length or

XX CC extracellular portions of GITRL together with full-length or

XX CC heterotrimeric complexes of other TNF ligand family members. The

XX CC heterotrimeric complexes of the invention are useful for treating an

XX CC autoimmune disease, cancer or osteoporosis, and particularly for

XX CC inhibiting cancer cell proliferation, increasing B cell proliferation, or

XX CC inducing apoptosis of T cells

XX SQ Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	3,01e-78	Length:	534
Score:	694.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

US-09-195-368-1_COPY_48_177 (1-130) x ACC57909 (1-534)

QY 1 PheleuglnleugluthrAlaIygluProCysMetAlaIySpheglProleuProser 20

DB 142 TTTCTCCATTAGAGACTGCTAAGAGCCCTGTATGCTTAAGTTGACCATTAACCTCA 201

QY 21 LysTrpGlnMetAlaSerSerGluProProCysValAsnIySerAspTrpIySleu 40

DB 202 AAATGGCAATAGGATCTTCTGAACCTCTTGCCTGATAGATGCTGAGGAGCTG 261

QY 41 GlulleuglnAsnglyLeuTyIleuIleTyIyGlnValAlaProAsnAlaAsnTy 60

DB 262 GAGATACCTTCAGATGCTTATATTATTTATGCGCAATGCTCCCAATGCAAACTAC 321

QY 61 AsnAspValAlaProPhegluValArgleuTyIyAsnIyAspMetIleGlnThrIleu 80

DB 322 AATGATGAGCTCTTTGAGTGGCTGTATTAACAAAGACATGATACCAACTCA 381

QY 81 ThrAsnIySerIyIleGlnAsnValIyGlyThyTyIyGlnIleuHisValIyAspThr 100

DB 382 ACAACCAATCTAATCAAAATGAGAGGAGGACTTATGATGCTGTTGGGAGACCC 441

QY 101 IleAspIleuIlePheAsnSerGlnHisGlnValIleuIyAsnAsnTyTyTrpGlyIle 120

DB 442 ATGACTTGATATTCACACTGAGCATCAGGTTCTAATAAATAATACATACCTGGGATTC 501

QY 121 IleleuIleuAlaAsnProGlnPheIleSer 130

D6		500	ATTTTACTAGCAAAATCCCATTCACATCCTCC 531
	RESULT 3		
XX	ID	ADC35221	standard; cDNA; 534 BP.
XX	AC	ADC35221;	
XX	DT	18-DEC-2003	(first entry)
XX	DE		
XX	Human cDNA encoding TNF ligand family member #20.		
KM	ss; gene; human; tumour necrosis factor; TNF ligand; endokine alpha;		
KM	excessive bone resorption disorder; osteoporosis; Paget's disease;		
XX	arterial calcification.		
OS	Homo sapiens.		
FN	US2003100074-A1.		
XX			
PD	29-MAY-2003.		
PR	15-AUG-2002; 2002US-00218547.		
XX			
XX	16-AUG-2001; 2001US-0312542P.		
PR	30-OCT-2001; 2001US-0330761P.		
XX			
PA	(YUGG/) YU G.		
PA	(NIJJ/) NI J.		
PA	(ROSE/) ROSEN C A.		
PA	(NARD/) NARDELLE B.		
XX			
PI	Yu G, Ni J, Rosen CA, Nardelli B,		
DR	WPI; 2003-696072/66.		
XX	P-PsDB; ADC35222.		
PT	New Endokine alpha gene useful for preparing a composition for treating a		
XX	disease associated with excessive or insufficient bone resorption e.g.,		
XX	osteoporosis, Paget's disease or arterial calcification.		
PS	Disclosure; SEQ ID NO 39; 145bp; English.		
CC	The invention relates to an isolated nucleic acid molecule encoding a		
CC	tumour necrosis factor family ligand. A composition comprising the		
CC	isolated antibody or its fragment is used for treating an individual in		
CC	need of decreased level of endokine alpha activity. The endokine alpha		
CC	polypeptide present in a heteromeric complex is used for treating an		
CC	individual having a disorder associated with excessive bone resorption,		
CC	e.g. osteoporosis, Paget's disease or arterial calcification. Treating an		
CC	individual having a disorder associated with insufficient bone resorption		
CC	comprises administering an endokine alpha antagonist, which is the		
CC	antibody that binds specifically to endokine alpha polypeptide. The		
CC	present sequence represents a cDNA encoding a tumour necrosis factor		
XX	family ligand.		
SO	Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;		
	Alignment Scores:		
Oy	Pred. No.: 3,01e-78 Length: 534		
	Score: 694.00 Matches: 130		
	Percent Similarity: 100.00% Conservative: 0		
	Best local Similarity: 100.00% Mismatches: 0		
	Query Match: 100.00% Indels: 0		
	DB: 9 Gaps: 0		
US-09-195-368-1_COPY_48_177 (1-130) x ADC35221 (1-534)			
Oy	1 PhelendunleugluThralalysGiuProCyMetalalysPhneGLyProleuProSer 20		
D6	142 TTITCCAAATTAGAGAGTGTCTAAGAGGCCCTGTATGGCTTAAGTTTGACCATTAACCTCA 201		
Oy	21 LysTrgplnMetalaserSergIuPrPoProCyValaslnlyVasalserAspTrplyLeu 40		

Db	202	AAATGGCAANTGGCAATCTTCTGAACTCTTCGGTGAATAGAGTGTGACTGGAAGCTG	261
Oy	41	GIUILLLEuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaSerTyr	60
Db	262	GAAATCTCTTCAGAAATGGCTTAATTTAATTTATATGGCCAAAGGGCTCCCAATGCAAACTAC	321
Oy	61	AsnAspValAlaProPheGluValAlaArgLeuTyrTyrAsnLysAspMetIleGlnThrLeu	80
Db	322	AAATGATGTAGTACTCTTTTGAGTGGGGCTGTATATAAACAAGACAGATACAAACTCTA	381
Oy	81	ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr	100
Db	382	ACAAACAATCTAAATCCAAATATGAGAGGAGCTTATGATTCATTCATGTTGGGGACACC	441
Oy	101	IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnTyrTyrTrpGlyIle	120
Db	442	ATAGACTGTATATCTCACTCTAGACATCAGGTTCTTAATAAATAATACATCTGGGGATTC	501
Oy	121	IleLeuLeuAlaAsnProGlnPheIleSer	130
Db	502	ATTTTACTAGCAAAATCCCAATTCATCTCC	531
RESULT 4			
AAV19195	ID	AAV19195 standard; cDNA; 1809 BP.	
XX	AC	AAV19195;	
XX	DT	26-AUG-1998 (first entry)	
DE		Human endokine-alpha cDNA.	
KM		Endokine-alpha; cytokine; tumour necrosis factor; human;	
KM		immunomodulation; infection; cell proliferation; angiogenesis; tumour;	
KW		metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;	
KM		diagnosis; therapy; ds; ss.	
OS		Homo sapiens.	
XX	FP	Key	Location/Qualifiers
FT		CDS	53..562
FT			/+tag= a
XX	FN	W09807880-A1.	
PD		26-FEB-1998.	
XX	XX		
PE		16-AUG-1996; 96MO-US013282.	
XX	XX		
PR		16-AUG-1996; 96MO-US013282.	
XX	XX		
PA		(HUMA-) HUMAN GENOME SCI INC.	
XX	XX		
PI		Yu G, Ni J, Rosen CA;	
XX	XX		
DE		WPI; 1998-169182/15.	
DR		P-PSDB; AAM37847.	
PT		Nucleic acid encoding human endokine-alpha - useful for diagnosis and	
PT		treatment of tumour necrosis factor-related diseases.	
XX	XX		
PS		Claim 1; Fig 1A-B; 78pp; English.	
XX	XX		
CC		This isolated nucleic acid, deposited as ATCC 97640, codes for human	
CC		endokine-alpha (see AAM37847), a novel member of the tumour necrosis	
CC		factor (TNF) family of cytokines. It was isolated from a cDNA library	
CC		established from human striatum. Expressed sequence tags corresponding	
CC		to a portion of the endokine-alpha cDNA were also found in several	
CC		endothelial libraries and a foetal liver library. Isolation of the	
CC		nucleic acid allow production of recombinant endokine-alpha in	
CC		transformed host cells. Endokine-alpha may be involved in disorders of	
CC		immunomodulation, infection, cell proliferation, angiogenesis, tumour	


```

Db      290 GAGATCTTCAGATGCTTATTTATTTATGCGCAAGTGCTCCCAATGCAAACTAC 349
Qy      61 AenaspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
Db      350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATATAAACAAGACATGATACAACTCTA 409
Qy      81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
Db      410 ACAACAAATCTAAATCCAAATCTAGAGGACTTATGCAATGCACTTGGGACACC 469
Qy      101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyTyr 120
Db      470 ATGACTTGATATTCACCTCTGAGCATGAGTTCCTAAAAATATATACCTACTGGGGTATC 529
Qy      121 IleLeuLeuAlaAsnProGlnPheIleSer 130
Db      530 ATTTTACTAGCAAAATCCCAATTCATCTCC 559

RESULT 6
AA257314
ID      AA257314 standard; cDNA; 1849 BP.
XX
XX      AA257314;
AC
XX      03-APR-2000 (first entry)
DT
XX      Human endokine alpha protein encoding cDNA SEQ ID NO:1.
DE
XX      Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KM      immunomodulation; inflammation; cell proliferation; angiogenesis;
KM      tumour metastasis; apoptosis; sepsis; endotoxemia; ds.
XX
XX      Homo sapiens.
OS
XX      Key      Location/Qualifiers
FH      CDS      53..562
FT      /*tag= a
FT      /product= "endokine alpha"
FT
XX      US5998171-A.
XX      07-DEC-1999.
XX
XX      15-AUG-1997; 97US-00912227.
PF
XX      16-AUG-1996; 96US-0024058P.
XX
XX      (HUMA-) HUMAN GENOME SCI INC.
PA
XX      NI J, Rosen CA, Yu G;
PI
XX
XX      WPI; 2000-104608/09.
DR      P-PSDB; AA53061.
XX
XX      Isolated human endokine alpha gene useful as a diagnostic probes and
PT      primers.
XX
XX      Claim 3; Fig 1; 31pp; English.
XX
XX      The present sequence encodes human endokine alpha which is a member of
CC      the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
CC      protein and polynucleotides can be used in diagnostic and therapeutic
CC      methods concerning TNF family-related disorders. These include disorders
CC      associated with immunomodulation and inflammation, cell proliferation,
CC      angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia
XX
SQ      Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,72e-77      Length:      1849
Score:          694.00      Matches:      130
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0

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```

Query Match:      100.00%      Indels:      0
DB:              3      Gaps:      0
US-09-195-368-1_COPY_48_177 (1-130) x AA257314 (1-1849)

Qy      1 PheLeuGlnLeuGlnThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
Db      170 TTCTCCAAATATAGAGCTGCTAAGAGCCCTGTATGGCTAAGTTGGACCATTAACCTCA 229
Qy      21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
Db      230 AAATGGCAATGCGCATCTTCTGAACCTCTTGCGGTAGATAGGTCTGACTGGAACTG 289
Qy      41 GluIleLeuGlnAsnGlyLeuTyrLysIleTyrGlyGlnValAlaProAsnAlaSerTyr 60
Db      290 GAGATCTTCAGATGCTTATTTATTTATGCGCAAGTGCTCCCAATGCAAACTAC 349
Qy      61 AenaspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
Db      350 AATGATGTAGCTCCTTTTGAGGTGCGGCTGTATATAAACAAGACATGATACAACTCTA 409
Qy      81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThr 100
Db      410 ACAACAAATCTAAATCCAAATCTAGAGGACTTATGCAATGCACTTGGGACACC 469
Qy      101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTrpGlyTyr 120
Db      470 ATGACTTGATATTCACCTCTGAGCATGAGTTCCTAAAAATATATACCTACTGGGGTATC 529
Qy      121 IleLeuLeuAlaAsnProGlnPheIleSer 130
Db      530 ATTTTACTAGCAAAATCCCAATTCATCTCC 559

RESULT 7
AD11463
ID      AD11463 standard; cDNA; 1849 BP.
XX
XX      AD11463;
AC
XX      06-NOV-2003 (first entry)
DT
XX      Human endokine alpha cDNA.
DE
XX      human; endokine alpha; melanoma; sarcoma; tumour; tumour regression;
KM      infection; viral; bacterial; yeast; fungal; Toxoplasma gondii;
KM      Schistosoma mansoni; Listeria monocytogenes; tumour necrosis factor;
KM      TNF-related disorder; endokine alpha-related disorder; immunomodulation;
KM      inflammation; cell proliferation; angiogenesis; tumour metastasis;
KM      apoptosis; sepsis; endotoxemia; ss; gene.
XX
XX      Homo sapiens.
OS
XX      Key      Location/Qualifiers
FH      CDS      53..562
FT      /*tag= a
FT      /product= "Endokine alpha"
FT
XX      US200209198-A1.
XX      25-JUL-2002.
XX
XX      01-JUN-1999; 99US-00345790.
PF
XX      16-AUG-1996; 96US-0024058P.
XX
XX      15-AUG-1997; 97US-00912227.
XX
XX      (YUG/) YU G.
XX      (NIJ/) NI J.
XX      (ROSE/) ROSEN C A.
XX
XX      Yu G, Ni J, Rosen CA;
PI
XX      WPI; 2003-605663/57.

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DR P-RSDB; ADA11464.

XX Novel isolated endokine alpha polypeptide, a member of tumor necrosis
PT factor ligand family, and antibodies against the polypeptides, useful for
PT treating melanoma, sarcoma, and viral, bacterial, fungal infections.

PS Claim 5; Fig 1; 29pp; English.

CC The invention relates to an isolated human endokine alpha polypeptide. A
CC cell recombinant for the human endokine alpha polypeptide is useful for
CC producing the protein by recombinant techniques. The antigenic epitope
CC bearing peptides and polypeptides are useful to raise antibodies
CC including monoclonal antibodies. The peptides and antipeptide antibodies
CC are used in a variety of qualitative or quantitative assays for the
CC protein. The protein is useful for tumour targeting and thus used in
CC patients with melanoma and sarcoma for tumour regression and extension of
CC patient life-span through a local injection. The protein is also useful
CC for treating viral, bacterial, yeast, fungal and other infections e.g.,
CC Toxoplasma gondii, Schistosoma mansoni, Listeria monocytogenes etc. The
CC protein is also useful for treating other tumour necrosis factor (TNF)-
CC related disorders. The nucleic acid is useful as probes for gene mapping
CC by in situ hybridisation and for detecting expression of endokine alpha
CC gene in human tissue e.g. by Northern blot analysis. The nucleic acid is
CC also useful for diagnosing an endokine alpha-related disorder such as
CC disorders associated with immunomodulation and inflammation, cell
CC proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or
CC endotoxaemia. The antibody is useful diagnostically or therapeutically as
CC antagonists in the treatment of alpha and/or TNF-related disorders. The
CC antibody is also useful for purification of the protein. The antibodies
CC are useful for detecting the protein and for tracking the fate of various
CC regions of a protein precursor which undergoes post-translational
CC processing. The present sequence represents cDNA encoding human endokine
CC alpha.

XX Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.: 1,72e-77 Length: 1849
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Gaps: 0

DB: 8 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x ADA11463 (1-1849)

QY 1 PheLeuGlnLeuGluThraAlaGluProCysMetAlaLysPheGlyProLeuProSer 20
DB 170 TTTCGCAATTGAGACAGCTGTAAGAGCCCTGTAAGCTTGAAGCATTACCTCA 229
QY 21 LysTPIGlnMetAlaSerSerGluProCysValAlaMetLysValSerAspTyrIleu 40
DB 230 AATGCGAATGAGCATCTTCTGACCTCTCGGATTAAGGTGCTGATGAGAACTG 289
QY 41 GluIleLeuGlnAsnGlyLeuTyrIleuIleTyrGlyGlnValAlaProAsnAlaMetTyr 60
DB 220 GAGAACTCTCAAGAAAGCTTATATTATTAATGAGCAAGGCTCCCAATGCAACTAC 349
QY 61 AsnAPValAlaProPheGlnValArgLeuTyrLysAsnLysAspMetIleGlnThrIleu 80
DB 350 AATGATGAGCTCTTTGAGGTGGGCTGTAATAAACAAGACATATCAACTCA 409
QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyTyrGlyLeuHisValGlyAspThr 100
DB 410 ACAAACAATCTTAAATCCAAATATAGAGAGGACTTGTGATTCAGATGTGGGACACC 469
QY 101 IleAspLeuIlePheAsnSerGluHisGlnValIleuLysAsnAsnThrTyrTyrGlyIle 120
DB 470 AATGACTTGAATTCACCTGAGCATCAGGTCTCAAAAATATTAATCTACTGGGATTC 529
QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
DB 530 ATTTACTAGCAAAATCCCAATTCATCTCC 559

RESULT 8

ID ADCC01857 standard; cDNA; 1849 BP.

AC ADCC01857;

DT 18-DEC-2003 (first entry)

DE Human cDNA encoding Endokine alpha.

XX Human; se; gene; endokine alpha; tumour necrosis factor family; AIDS;
KW Chronic lymphocyte disorder; tumour; parasitic disease;
KW autoimmune disease; lupus; arthritis; multiple sclerosis; inflammation;
KW graft versus host disease; transplant rejection; skin allergy;
KW bowel disease; wound; sepsis; Hodgkin's disease;
KW chronic lymphocyte leukaemia; Burkitt's lymphoma; scleroderma;
KW chronic active hepatitis; myasthenia gravis; psoriasis;
KW autoimmune thyroiditis; Goodpasture's disease; acutima; Graves disease;
KW cirrhosis; insulin dependent diabetes mellitus; Sjogren's syndrome;
KW glomerulonephritis; hepatitis; Parkinson's disease; atherosclerosis;
KW rheumatoid arthritis.

XX Homo sapiens.

FT Key Location/Qualifiers
FT CDS 53..562
FT /tag=a
FT /product="Endokine alpha"

PN US2002168729-A1.

PD 14-NOV-2002.

PF 02-MAY-2002; 2002US-00136511.

XX 16-AUG-1996; 96US-0024058P.

PR 15-AUG-1997; 97US-00912227.

PR 26-FEB-1999; 99US-0122099P.

PR 28-MAY-1999; 99US-0136788P.

PR 01-JUL-1999; 99US-00345790.

PR 25-FEB-2000; 2000US-00513584.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Yu G, Ni J, Rosen CA;

PI WPI; 2003-755028/71.

XX Novel isolated endokine alpha polypeptide AIDS, chronic lymphocyte

PT disorder, common variable immunodeficiency, a tumor, parasitic disease,

PT autoimmune disease, lupus, arthritis, multiple sclerosis.

XX Claim 1; SEQ ID NO 1; 90pp; English.

XX The invention relates to an isolated endokine alpha polypeptide (a member
CC of the tumour necrosis factor family), appearing as ADCC01858, the
CC sequence of the endokine alpha polypeptide having an sequence encoded by
CC the cDNA clone contained in ATCC Deposit number 97640 (A1) and the
CC sequence of an epitope-bearing portion of the above polypeptides. Also
CC included are the encoding nucleic acid (its homologues, complements or
CC fragments where the fragment comprises at least 50 contiguous
CC nucleotides), provided that the fragment is not from a region starting at
CC nucleotide 26 and ending at nucleotide 476 of ADCC01857), making a
CC recombinant vector comprising the nucleic acid and an isolated antibody
CC or antibody fragment that binds specifically to endokine alpha. The DNA
CC and protein are useful for treating an individual having a disorder
CC chosen from AIDS, chronic lymphocyte disorder, common variable
CC immunodeficiency, a tumour, parasitic disease, autoimmune disease, lupus,
CC arthritis, idiopathic thrombocytopenic purpura, multiple sclerosis,
CC chronic inflammation, acute inflammation, acute allograft rejection,
CC graft versus host disease, transplant rejection, foetal resorption,
CC faecal peritonitis, skin allergies, bowel disease, a wound, sepsis, ATL,

CC Hodgkin's disease, non-Hodgkin's lymphoma, chronic lymphocytic leukaemia
CC plasmacytomas, multiple myeloma, Burkitt's lymphoma, EBV-transformed
CC disease, chronic myelogenous leukaemia, chronic hypercarnitine/phenylalaninaemia
CC autoimmune haematological disorders, polychondritis, scleroderma, Wegner's
CC granulomatosis, dermatomyositis, chronic active hepatitis, mastocytosis
CC graves, peoria/sis, Steven-Johnson syndrome, idiopathic spine, autoimmune
CC thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive
CC enteropathy, autoimmune neutropenias, pemphigus vulgaris, Goodpasture's
CC disease, bullous pemphigoid, discoid lupus, dense deposit disease,
CC endocrine ophthalmopathy, IBD, asthma, Graves disease, sarcoidosis,
CC cirrhosis, juvenile diabetes, insulin dependent diabetes mellitus,
CC cystitis, autoimmune gastritis, lymphopneumonia, olivary/teritis nodosa,
CC Sjögren's syndrome, Becker's disease, Hashimoto's disease, primary
CC myxoedema, polyarthritis, mixed connective tissue disease, primary
CC keratoconjunctivitis sicca, vernal keratoconjunctivitis, interstitial
CC lung fibrosis, glomerulonephritis, hepatitis, autoimmune haemolytic
CC anaemia, contact sensitivity diseases, Parkinson's disease, primary
CC lateral sclerosis, spondylosis, sarcoidosis, idiopathic pulmonary fibrosis
CC idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis
CC histamine-mediated allergic reactions, IgE-mediated allergic reactions,
CC rheumatoid arthritis, plastic anaemia and myelodysplastic syndrome. The
CC present sequence encodes Enothrine alpha.

SQ Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1,72e-77	Length:	1845
Score:	694.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-195-368-1_COPY_48_177 (1-130) X ADC01857 (1-1849)

QY 1 PhenendineugitrritalalysgiuprocymetalalysphagiProleupser 20
DB 170 TTTCTCCAAATTAGAGCTGTAGAGACCCTGATAGCTAGTTGGACATTACCTCA 22
QY 21 LysTrpGlnMetalaserSergiuproProcysalasnValSerAspTrpLysIeu 40
DB 230 AAATGGCAAAATGGCATCTTCTGAACCTCCTTGAGTAATAGTGTGACTGGAGCTG 28
QY 41 GluIleuIeuGlnasnGlyLeuTyrlleuIleTyrglyGlnValAlaPProasnAlaasntTyr 60
DB 290 GAGATACTTGAAGATGGCTTAATTTAATTTATGGCAAGTGGCTCCCAATGGCAACACTAC 34
QY 61 AsnAspValAlaPProPegiValAlaArgLeuTyrlAsnLysAspMetIleGlnThrIeu 80
DB 350 AATATGTTAGCTCCTTTTGGAGTGGCGGCTGTATATAAACAAAGACATATATCCAACTCTA 40
QY 81 ThrAsnLysSerLysIleGlnasnValIgiGlyTyrlThrTyrlGluLeuHisValIgiYAspThr 100
DB 410 ACACAACAATCTAAATATCCAAATATGlnGAGGGAGACTTATGAATTCAGTGTGGGAGACCC 46
QY 101 IleaspLeuIlePheasnSerGluHisGlnValLeuLysAsnAsnThrTyrlTrpGlyIle 120
DB 470 ATGACACTTGATATTCAACTCTGAGCATCGAGGTCTTAAAAATAATATACCTACTGGGGATAC 52
QY 121 IleuIeuLeuAlaasnpGlnPheIleSer 130
DB 530 ATTTTACTGCAAAATCCCAATTCATCTCC 559

RESULT 9

ID AAX59844 standard; cDNA; 1964 BP.

AC AAX59844;
VV

DT 28-JUL-1999 (first entry)

CDNA sequence for human DNA19355.

KM DNA19355; tumour necrosis factor homologue; receptor G1T6; immunogen;
KM antibody; apoptosis; mamalian cancer cell;
KM tumour necrosis factor (TNF)-alpha secretion; primary T- cell;
KM proinflammatory response; ds.

OS Homo sapiens

PN WO9925834-A1
 VV

PD 27-MAY-1999.
XY

PF 18-NOV-1998; 98MO-US024621.
XX

PR 18-NOV-1997; 97US-0065635P
PR 12-DEC-1997; 97US-0069661P

XX
PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Gurney

DOCUMENT FOR DATA USE

DR P-PSDB; AAY15817.

PT New DNA19355 polypeptide as tumour necrosis factor homolog

Example 1; Fig 1; 86pp; English.

The present sequence encodes a p

The present disclosure encodes a polypeptide or a fragment thereof, and the polypeptide is a tumour necrosis factor homologue. The DNA1935 polynucleotide sequence can be used to derive hybridisation probes for e.g. isolating similar sequences, gene mapping, genetic analysis, etc. Nucleic acids which encode DNA1935 can also be used to generate transgenic or knockout animals, which are useful in the development and screening of therapeutically useful reagents. The DNA1935 polypeptides may be used in diagnostic assays to detect the presence of the receptor GTR in mammalian tissues. The polypeptides can also be used as immunogens to raise antibodies. The polypeptides may also be used to induce apoptosis in mammalian cancer cells. DNA1935 polypeptides stimulate secretion of tumour necrosis factor (TNF- α) in primary T cells, and so can be used to stimulate a proinflammatory response in mammalian cells.

SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other

Alignment Scores:

Pred. No.:	1,87e-77	Length:	196
Score:	634.00	Matches:	130
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-195-368-1_COPY_48_177 (1-130) X AAX59844 (1-1964

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Oy PhleuGlnuGlnuThrlAlayGluProCyMetAlaLysPheGluProLeuProSer 20
Db 162 TTTCTCCATTAAAGCTCTTAAGAGCCCTTAAGCTTAAGTTGGACATTACCTCA 22
Oy 21 LysTfGlnMetLaseSerGluProProCyValAsnLysValSerAspTrpLysLeu 40
Db 222 AAATGGCAATGGCACTTCTTAACCTCTTGCGGAAATAAGGTGTCACTGGAAAGTG 28
Oy 41 GlnLLeuGlnAsnGlyLeuTrpLeuLleTrpGlyGlnValAlaProAsnAlaSerTrp 60
Db 282 GAAATCTCTCAGATAGCTTATATTATTTATTTATGGCCCAAGTGCCCTCCAAAGCAACATAC 34
Oy 61 AsnAspValAlaProPheGlnValAlaGlnLeuTrpLysAsnLysAspMetLlGlnThrLeu 80
Db 342 AATGATGTAGCTCTTTTGAAGTGCGCGCTGTATTAACCAAGACATATATCAAACTCTA 40
Oy 81 ThrAsnLysSerLysLlGlnAsnValGlyGlyThrTrpGluLeuHisValGlyAspThr 100

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Db      402 ACAACAAATCTAAATCCAAAATGTAGAGGAGCTTATGATTGCTGTTGGGACACC 461
Qy      101 IleaPleuIlePheAsnSerGluHISGlnValIleuLysAsnGlnThrTyTTPGlyIle 120
Db      462 ATAGACTTGATATTCACCTCTGACGATCAGGTTCTAAATAATATACATCTGGGGTATC 521
Qy      121 IleaPleuAlaAsnProGlnPheIleSer 130
Db      522 ATTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 10
AAx87726 standard; cDNA; 1964 BP.
ID      AAx87726 standard; cDNA; 1964 BP.
AC      AAx87726;
XX      26-OCT-1999 (first entry)
DT      26-OCT-1999 (first entry)
XX      Human PRO364 ligand cDNA clone DNA19355-1150.
DE      XX
KW      PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
KM      inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
XX      therapy; ds.
XX      Homo sapiens.
OS      Homo sapiens.
XX      Key
FH      Location/Qualifiers
FT      CDS
FT      21..554
FT      /*tag= a
XX      WO9940196-A1.
XX      12-AUG-1999.
XX      09-FEB-1999; 99MO-US002642.
XX      09-FEB-1998; 98US-0074087P.
XX      09-FEB-1998; 98US-0074087P.
XX      (GETH ) GENENTECH INC.
XX      Ashkenazi AJ, Gurney AL, Marsters SA, Pillei RM, Wood WI;
PI      Goddard A;
XX      WPI; 1999-494296/41.
XX      P-PSDB; AAy06646.
XX      DR
XX      Tumor necrosis factor receptor homologue - useful for, e.g. modulating
PT      apoptosis and NF-KB activation and proinflammatory or autoimmune
PT      responses.
XX      Example 2; Fig 5A-B; 104pp; English.
XX      This is the nucleotide sequence of a novel cDNA clone, termed DNA19355-
CC      1150 (ATCC 209466), coding for a potential ligand (see AAy06646) of
CC      PRO364 (see AAy06605), a novel member of the tumour necrosis factor
CC      receptor family. The clone was isolated from a human umbilical vein
CC      endothelial cell cDNA library constructed in yeast transformants. PRO364
CC      polypeptides are useful for modulating apoptosis, NF-KB activation and
CC      proinflammatory or autoimmune responses in mammalian cells (claimed).
XX      SQ      Sequence 1964 BP; 596 A; 370 C; 380 G; 616 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:      1.87e-77      Length:      1964
Score:          694.00      Matches:      130
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              2      Gaps:      0

US-09-195-368-1_COPY_48_177 (1-130) x AAx87726 (1-1964)
Qy      1 PheLeuGlnLeuGlnThrAlaLysGlnProCysMetAlaLysPheGlyProLeuProSer 20

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Db      162 TTCTCCATTTGAGACTGCTTGAAGAGCCCTGTATGTTAGTTGACCTTACCTCA 221
Qy      21 IyTTPGlnMetAlaSerSerGluProCysValAsnLysValSerAspTyrLysLeu 40
Db      222 AAATGGCAAAATGCATCTTCTGAACCTCCTTGCGGATAAGGTGTGACTGGAGCTG 281
Qy      41 GlnIleuGlnAsnGlyLeuTyrIleuIleTyrGlyGlnValAlaProAsnAlaAspTyr 60
Db      282 GAGATACCTTGAAATGGCTTATTTATTTATTTATGCGCAAGTGGCTCCCAATGCAACTAC 341
Qy      61 AsnAspValAlaProPheGlnValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
Db      342 AATGATGATAGCTCCTTTGAGGTGGGCTGTATATAAACAAGACATGATCAAACTCTA 401
Qy      81 ThrAsnLysSerIyIleGlnAsnValIleGlyIleTyrGlnLeuIleValGlyAspThr 100
Db      402 ACAACAAATCTAAATCCAAAATGTAGAGGAGCTTATGAAATGCAATGTTGGGACACC 461
Qy      101 IleaPleuIlePheAsnSerGluHISGlnValIleuLysAsnGlnThrTyTTPGlyIle 120
Db      462 ATAGACTTGATATTCACCTCTGACGATCAGGTTCTAAATAATATACATCTGGGGTATC 521
Qy      121 IleaPleuAlaAsnProGlnPheIleSer 130
Db      522 ATTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 11
AAc85435 standard; cDNA; 1964 BP.
ID      AAC85435 standard; cDNA; 1964 BP.
AC      AAC85435;
XX      08-MAY-2001 (first entry)
DT      08-MAY-2001 (first entry)
XX      Clone PRO175-1150.
XX      PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
KM      hGTR; ligand; hGTR; PRO175; tumour necrosis factor receptor; TNFR;
KM      human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
KM      myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis;
KM      age-related macular degeneration; antibody; periodontal disease;
KM      vascular-related drug targeting; atherosclerosis; hypertension;
KM      inflammatory vasculitides; Reynaud's disease; aneurysm;
KM      arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
KM      fibrosis; neuropathy; rheumatoid arthritis; ss.
XX      Homo sapiens.
XX      OS
XX      Key
FH      Location/Qualifiers
FT      CDS
FT      21..554
FT      /*tag= a
FT      /product= "PRO175"
XX      WO200103720-A2.
XX      18-JAN-2001.
XX      11-JUL-2000; 2000MO-US018867.
XX      12-JUL-1999; 99US-0143304P.
XX      (GETH ) GENENTECH INC.
XX      Williams PM, Gerritsen ME;
PI      WPI; 2001-138257/14.
XX      P-PSDB; AA847056.
XX      DR
XX      Composition for diagnosing and treating cardiovascular, endothelial and
PT      angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
XX      Example 2; Fig 5; 76pp; English.
XX      PS

```


CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies, and a method of stimulating an immune response in a mammal
CC using PRO179

Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:	
Pred. No.:	1.87e-77
Score:	64.4
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	4
Length:	1964
Matches:	130
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-195-368-1_COPY_48_177 (1-130) X AAF30051 (1-1964)

QY	PhleuGlnIleuInuThiAlaLysGluProCysMeAlaLysPheGluProIleuProSer	20
Db	162 TTTCTCCAAATTAAAGACTGCTAAGAGCCCTTAAGCTTAAGCTTTGGACCATTAACCTCA	22
QY	21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysIleu	40
Db	222 AAATGGCAATGGCACTCTTCTGAACCTCTTCGGTAATAAAGTGTCTGACTGGAAAGCTG	28
QY	41 GlnIleIleuGlnAsnGlyLeuTyIleuLeuIleTyIleTyGlnValAlaIleProAsnAlaAsnTyr	60
Db	282 GAAATACCTTCAGATAGGCTTATATTAAATTATGGCCAAAGGGCCCAATGGCAAACTAC	34
QY	61 AsnAspValAlaProPheGluValArgLeuTyIleLysAsnLysAspMetIleGlnThrIleu	80
Db	342 AATGACGTAGACTCTTTTGAAGTGGCGCGCTGTATAAACAAAGACATATATCAAACTCTA	40
QY	81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyGluLeuIleValAlaIleAspThr	100
Db	402 ACAACCAATCTAAATCCAAATGTAAAGAGGAGCTTGAATTGCAGTTGGGGGACACC	46
QY	101 IleAspLeuIlePheAsnSerGluIleIleGlnValLeuLysAsnAsnThrTyIleTrpGlyIle	120
Db	462 ATGACCTTGATTATCAACTGTGAGCATCGGTTCTAAAAAAATTAATACACTACTGGGGTATC	52
QY	121 IleLeuLeuAlaAsnProGlnPheIleSer	130
Db	522 ATTTTACTAGCAAAATCCCAATTCATCTCC	551

RESULT 13

ID AAC97374 standard; cDNA; 1964 BP.

AC AAC97374

DT 28-FEB-2001 (first entry)

DE Human angiogenesis-associated protein PRO175 cDNA, SEQ ID NO:8.

KM Human; atherosclerosis-associated protein; PBC; endothelial cell growth;
 KM cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KM angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KM myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KM Crohn's disease; psoriasis; endotheliolysis; ulcer; wound healing; cancer
 KM Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KM gene therapy; transgenic animal; ss.

OS Homo sapiens.

PN W0200053753-A2.

PD 14-SEP-2000

PF 05-JAN-2000; 2000WO-US0000219.

PR 08-MAR-1999; 99WO-US005028.

PR	12-MAR-1999;	99US-0123957P.
PR	14-MAY-1999;	99US-0134287P.
PR	02-JUN-1999;	99MO-US012252.
PR	23-JUN-1999;	99US-0141037P.
PR	20-JUL-1999;	99US-0144758P.
PR	26-JUL-1999;	99US-0145698P.
PR	01-SEP-1999;	99MO-US020111.
PR	08-SEP-1999;	99MO-US020594.
PR	15-SEP-1999;	99MO-US02190.
PR	15-SEP-1999;	99MO-US021547.
PR	05-OCT-1999;	99MO-US023089.
PR	30-NOV-1999;	99MO-US028313.
PR	30-NOV-1999;	99MO-US028409.
PR	02-DEC-1999;	99MO-US028564.
PR	02-DEC-1999;	99MO-US028565.

PA (GETH) GENENTECH INC

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;

PI Paoni NF, Pitti RM,

DR. WPI; 2001-090793

PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT genetic disorders and treating cardiovascular, endothelial or angiotensin
PT disorders, such as atherosclerosis, wounds or cancer.

PS Claim 58; Fig 3A-B; 293pp; English

The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a cDNA encoding a PRO protein of the invention.

Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

Score:	694.00	Matches:	130
--------	--------	----------	-----

Best Local Similarity: 100.00% Mismatches: 0

DB:	4	Gaps:

US-09-195-368-1_COPY_48_177 (1-130) x AAC97374 (1-1964)	
QY 1	PheLeuGlnLeuGlnThrAlaValGluProCysMetAlaValPheGlyProLeuProSer 20
Db 162	TTTTCTCCAAATTAAAGACTCTTAAGGAGCCCTGTATGGTAAAGTTTGACCATTAACCTCA 221
QY 21	LVeTrpGlnMetAlaSerSerGluProProCysValaIasnValaSerAspTrpLysLeu 40
Db 222	AAATGGCAATGGCACCCTCTTGACACTCTTCGCGAATTAAGGTGTGACTGGAACTG 281
QY 41	GluIleLeuGlnAsnGlyLeuTyrlleuIleTyrlGlyGlnValAlaProAsnAlaAspTyr 60
Db 282	GAGTACTCTTGAGATGGCTTATATTATTTATGGCCAAAGGCGCTCCCAATGCCAACTAC 341
QY 61	AsnAspValAlaProPheGluValArgLeuTyrlLysAsnLysAspMetIleGlnThrLeu 80
Db 342	AATGATTAACCTCTTTTGGAGCGCGCTGTATTAACCAAGACATGATACAACTCA 401
QY 81	ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrlGluLeuHisValGlyAspThr 100
Db 402	ACAAACAAATCTAAATCCAAATGAGAGAGGACTTATGATTAATGACATGGGGGACACC 461
Db 101	IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrlTrpGlyIle 120
Db 462	ATAGACTGTATTCACTGACCTGAGCATCGGTCTTAAAAAATATACATACTGGGATTC 521
QY 121	IleLeuLeuAlaAsnProGlnPheIleSer 130
Db 522	ATTTTACTACGAATCCCAATTCATCTCC 551
RESULT 14	
AAC85945	
ID AAC85945	standard; cDNA; 1964 BP.
XX AC AAC85945;	
XX DT 22-AUG-2001	(first entry)
XX Native sequence of PRO175 cDNA, clone DNA19355-1150-1.	
KM PRO; type II transmembrane protein; tumour necrosis factor; stroke;	
KM heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;	
KM myocardial infarction; cardiac hypertrophy; RGF_2alpha; trauma; bone;	
KM cancer; age-related macular degeneration; wound burn; hypertension;	
KM diabetes mellitus; osteoporosis; ischemia; atherosclerosis; psoriasis;	
KM rheumatoid arthritis; Crohn's disease; amyotrophic lateral sclerosis;	
KM endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;	
KM Alzheimer's disease; Parkinson's disease; Huntington's disease; se.	
XX Homo sapiens.	
XX CS	
FH Key	Location/Qualifiers
FT CDS	16..554
FT FT	/*tag= a
FT sig_peptide	/product= "PRO175 polypeptide"
FT FT	16..95
FT mat_peptide	/*tag= b
FT FT	96..551
FT FT	/*tag= c
XX MO200140464-A1.	
XX PD	
XX 07-JUN-2001.	
XX PF	
XX 11-AUG-2000; 2000OWO-US022031.	
XX PR	
XX 30-NOV-1999; 99OWO-US028313.	
XX PR	
XX 30-NOV-1999; 99OWO-US028409.	
XX PR	
XX 05-JAN-2000; 2000OWO-US000219.	
XX PR	
XX 24-FEB-2000; 2000OWO-US005004.	
XX PR	
XX 15-MAR-2000; 2000OWO-US006884.	
XX PR	
XX 30-MAR-2000; 2000OWO-US008439.	
XX PR	
XX 17-MAY-2000; 2000OWO-US013705.	

Db 522 ATTACTAGCAATCCCCAATTCATCTCC 551

RESULT 15

ID AAC90563 standard; cDNA, 1964 BP.

XX AAC90563;

XX 21-MAR-2001 (first entry)

XX Human PRC175 cDNA.

XX Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;

XX vasotrophic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;

XX vulnerrary; antianginal; gene therapy; cardiovascular disease;

XX endothelial disorder; angiogenic disorder; cancer; periodontal disease;

XX wound healing; ss.

XX Homo sapiens.

XX MO200073445-A2.

XX 07-DEC-2000.

XX 17-MAY-2000; 2000WO-US013705.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144568P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 01-SEP-1999; 99WO-US020111.

XX 30-NOV-1999; 99WO-US028313.

XX 02-DEC-1999; 99WO-US028409.

XX 16-DEC-1999; 99WO-US028565.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 24-FEB-2000; 2000WO-US005004.

XX 02-MAR-2000; 2000WO-US005841.

XX 10-MAR-2000; 2000WO-US006319.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000WO-US007532.

XX 30-MAR-2000; 2000WO-US008439.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gertlesen ME;

XX Goddard A, Goddard PJ, Gurney AL, Kuo SS, Mark MR, Marsters SA;

XX Paoni NF, Pilti RM, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2001-025251/03.

XX P-PSDB; AAB50951.

XX Seventeen nucleic acids encoding PRO polypeptides which are useful in

XX diagnosis and treatment of cardiovascular, endothelial or angiogenic

XX disorders in a mammal.

XX Claim 60; Fig 1; 182pp; English.

CC are also used to stimulate wound healing and tissue regeneration. The PRO

CC nucleic acids, polypeptides and anti-PRO antibodies are useful for

CC diagnosing a cardiovascular, endothelial or angiogenic disorder

XX SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

XX Alignment Scores:

XX Pred. No.:

XX Score:

XX Percent Similarity:

XX Best Local Similarity:

XX Query Match:

XX DB:

XX US-09-195-368-1_COPY_48_177 (1-130) x AAC90563 (1-1964)

XX QY 1 PheLeuGlnLeuGluThAlaLysGluProCySmetAlaLysPheGlyProLeuProSer 20

XX Db 162 TTTCGCAATAGAGAGCTAAGAGGCTGATGCTAGTTGACCAATACCTCA 221

XX QY 21 LysTPGImetAlaSerSerGluProProCySmetAlaLysValSerAspTyrLysLeu 40

XX Db 222 AAATGGCAATGGCATCTTCTGAACTCTTGGGATAGGTGTGACTGGAGCTG 281

XX QY 41 GluIleuGlnLeuGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60

XX Db 282 GAGATACCTCAGAAAGGCTTATTTATTTATGCGCAAGGCTCCCAATGCAAACTAC 341

XX QY 61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80

XX Db 342 AATGATGATGCTCTTCTTGAAGTGGCTGTATTAACCAAGACATATCAAACTCA 401

XX QY 81 ThrAsnLysSerLysIleGlnAsnValGlyTyrTyrGluLeuHisValGlyAspThr 100

XX Db 402 ACAACCAATCTAAATCCAAATGATAGAGGACTTATGATTCATGCTGGGACAC 461

XX QY 101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAsnThrTyrTyrGlyLe 120

XX Db 462 ATGAGCTGATATTAATCTGAGCATCAAGTCTTAAATAATATCACTAGGAGTATC 521

XX QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130

XX Db 522 ATTACTAGCAATCCCCAATTCATCTCC 551

Search completed: April 7, 2004, 17:08:51
Job time : 236.205 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 16:50:59 ; Search time 1779.77 Seconds

(without alignments)
2181.225 Million cell updates/sec

SUMMARIES

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Title: us-09-195-368-1_copy_48_177
Perfect score: 694
Sequence: 1 FLOJETAKEPCMAKFGPLPS.....VLKNNYWGIIILANPQIS 130
Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

MODEL=frame_plus_p2n.model -DEV=xl
-O=/cgn2.1/USPFO_spool_p/US09195368/runat_07042004_061638_2636/app_query.fasta_1.654
-DB=BST -QFMT=fastap -SUFFIX=rst -WINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=U09195368 -CGN 1.1 5436 @runat_07042004_061638_2636 -MCPU=6 -ICPU=3
-NO_MMAR -LARGESUBSTRY -NEG.SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV.TIMEOUT=120 -MARN.TIMEOUT=30 -THRADs=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: em_hic1.*
10: gb_est1.*
11: gb_est2.*
12: gb_hic.*
13: gb_est3.*
14: gb_est4.*
15: gb_est5.*
16: em_estfun.*
17: em_estom.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_plin.*
21: em_gss_vit.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_png.*
27: em_gss_vrl.*
28: gb_gss1.*

Result *
No. Score Match Length DB ID

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2	608	87.6	669	29	AG189267	AG189267 Pan trogl
3	294	42.4	350	13	BY216375	BY216375 BY216375
4	240	34.6	348	13	BY216375	BY216375 BY216375
5	138	19.9	334	13	BY326400	BY326400 BY326400
6	127	18.3	328	13	BY326606	BY326606 BY326606
7	123	17.7	324	13	BY327839	BY327839 BY327839
8	117	16.9	324	13	CG977950	CG977950 CH240.168
9	110	15.9	324	13	CG977950	CG977950 CH240.168
10	110	15.9	324	13	CG977950	CG977950 CH240.168
11	88	12.7	638	9	AT982044	AT982044 Pat. PK007
12	87.5	12.6	855	13	EX843917	EX843917 BX843917
13	85	12.2	575	13	BM232049	BM232049 BM232049
14	85	12.2	878	29	CG463627	CG463627 ZUHXK11TV
15	84.5	12.2	814	28	BZ758026	BZ758026 PUDBK49TD
16	84	12.1	564	13	BM091647	BM091647 BM091647
17	84	12.1	566	9	AV895903	AV895903 AV895903
18	84	12.1	682	9	AV854531	AV854531 AV854531
19	84	12.1	694	9	AV894346	AV894346 AV894346
20	84	12.1	720	13	BM299761	BM299761 BM299761
21	84	12.1	726	13	BM169798	BM169798 BM169798
22	84	12.1	728	13	BM169887	BM169887 BM169887
23	84	12.1	729	13	BM169841	BM169841 BM169841
24	84	12.1	746	13	BM175773	BM175773 BM175773
25	84	12.1	771	13	BM062488	BM062488 BM062488
26	83	12.0	470	9	AT168441	AT168441 OK30908.X
27	83	12.0	823	14	CF831057	CF831057 UCRCS01.0
28	82.5	11.9	602	13	BM305081	BM305081 BM305081
29	82.5	11.9	800	12	BG246328	BG246328 602355119
30	82	11.8	358	10	BR121624	BR121624 601757130
31	81.5	11.7	973	28	BZ967128	BZ967128 PUDBS30TD
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ALIGNMENTS

RESULT 1
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DEFINITION BX473859 634 bp mRNA linear EST 04-SEP-2003
DKEP686K13165.r1 686 (synonym: hicc3) Homo sapiens cDNA clone
DKEP686K13165 5', mRNA sequence.
ACCESSION BX473859
VERSION BX473859.1 GI:316688103
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 634)

AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Well, B., Amid, C., Oesanger, A.,
TITLE FobO, G., Han, M. and Wiemann, S.
JOURNAL Est (Bahr, A., Lauber, J., Mewes, H.W., Well, B., et al.)
 Unpublished (2003)
COMMENT Contact: MIPS
 MIPS

FEATURES
 source
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by Oigen (Hilden/Germany) within the CDNA sequencing
 consortium of the German Genome Project.
 No 5' sequence available.
 This clone (DKFZp686K13165) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
 Location/Qualifiers
 1..634
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ORIGIN

Alignment Scores:
 Pred. No.: 7,43e-76 Length: 634
 Score: 694.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x BX473859 (1-634)

ORIGIN
 1 PheleugluuGluThAlaAlaGluProCysMetAlaLysPheGlyProLeuProSer 20
 186 TTTCCTCAATGAGACATGCTAGAGAGCCCTGATGAGCTTAAGTGGACCTTAACCCCA 245
 21 LysTGTGMeAlaSerSerGluProCysValaLysValaSerAspTyrLysLeu 40
 246 AATGGCAATGCGATCTTCTGAACCTCTGCGGATTAAGTGTCTGATGAGAGCTG 305
 41 GluileuGluAsnGlyLeuTyrLeuileTyrGlyGluValaAlaProAsnAlaAsnTyr 60
 306 GAGATACCTCAGAAAGGCTTATTTATTTATGCGCAAGTGGCTCCCAATGCAAACTAC 365
 61 AsnAspValaAlaProPheGluValaArgLeuTyrLysAsnLysAspMetileGlnThrLeu 80
 366 AATGATGATGCTCTTTGAGCTGCGCTGCTATTAACCAAGACATATCAAACTCTA 425
 81 ThrAsnLysSerLysileGlnAsnValaGlyGlyThrTyrGluLeuHisValaGlyAspThr 100
 426 ACAAACAATCTMAAATCCAAATATGAGAGGAGCTTATGAATTCAGATGTTGGGACACC 485
 101 ileAspLeuilePheAsnSerGluHisGluValaileLysAsnAsnThrTyrTyrGlylle 120
 486 AARGACTTATATCAACTCTGAGCATCGAGTTCTTAAATAATTAATCACTAGGGGATTC 545
 121 ileLeuLeuAlaAsnProGlnPheileSer 130
 546 ATTCTACTAGCAAAATCCCAATTCATCTCC 575

RESULT 2
 AG182677 669 bp DNA linear GSS 09-JAN-2002
 AG182677
 LOCUS Pan troglodytes DNA, clone: RP43-055022.T7, genomic survey
 DEFINITION
 ACCESSION AG182677

VERSION AG182677.1 GI:16712357
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE
 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library RPCI-43
 Unpublished
 2 (bases 1 to 669)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
 end was generated during the R&D process and may have higher chance
 of clone tracking errors.

COMMENT

PRIMERS
 Sequencing: T7
 Library
 Vector : pBAC3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI

FEATURES

source
 1..669
 Location/Qualifiers
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 /db_xref="taxon:9598"
 /clone="RP43-055022.T7"
 /sex="male"
 /cell_type="lymphocytes"
 /clone_lib="RPCI-43 Chimpanzee Male BAC Library"

ORIGIN

Alignment Scores:
 Pred. No.: 4.17e-65 Length: 669
 Score: 608.00 Matches: 114
 Percent Similarity: 95.04% Conservative: 1
 Best Local Similarity: 94.21% Mismatches: 6
 Query Match: 87.61% Indels: 0
 DB: 29 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AG182677 (1-669)

ORIGIN
 10 ProCysMetAlaLysPheGlyProLeuProSerLysTyrGlnMetAlaSerSerGluPro 29
 258 CTTGATATTTCTTACAGACCATTAACCTCAAAATGGCAATGCGATCTTGAACCT 317
 30 ProCysValaAsnLysValaSerAspTyrLysGluileLeuGluAsnGlyLeuTyrLeu 49
 318 CTTGGGTGAATAGGATGCTGAGAGCTGAGATCTTCAAGATGCTTATTTTA 377
 50 ileTyrGlyGluValaAlaProAsnAlaAsnTyrAsnAspValaAlaProPheGlyValaArg 69
 378 ATTATGGCGCAAGTGGCTCCCAATGCAACTCAATGATGATGTTGCTTTGAGGCGG 437
 70 LeuTyrLysAsnLysAspMetileGlnThrLeuThrAsnLysSerLysileGlnAsnVal 89
 438 CTGTATTAACCAAGACATGATACCAACTCTAACAACCAAAATCTTAAATCCAAATGTA 497
 90 GlyGlyThrTyrGluLeuHisValaGlyAspThrileAspLeuilePheAsnSerGluHis 109
 498 GAGGGACCTTAATGATGCTGTTGGGACACCATGACCTAGATATTAACTCTGAGCAT 557
 110 GlnValaileLysAsnAsnThrTyrTyrGlylleileLeuLeuAlaAsnProGlnPheile 129
 558 CAGGTTCTAATAAATAATATCACTGAGGATCATTTTACTAGCAAAATCCCAATTAAT 617

QY 130 Ser 130
Db 618 TCC 620

RESULT 3
BY216375

LOCUS BY216375 350 bp mRNA linear EST 10-DEC-2002

DEFINITION BY216375 RIKEN full-length enriched, activated spleen Mus musculus

ACCESSION BY216375

VERSION BY216375.1 GI:26397123

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nakado, I., Oseco, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojodori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brad, E., Bruscia, V., Chothia, C., Corbett, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltas, L., Marchionni, L., McKenzie, L., Mikli, H., Nagashima, T., Numa, K., Okido, T., Pavan, W. J., Petras, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sanderlin, A., Schneider, C., Sempke, C. A., Secot, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Vitarito, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wymshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, R., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, K., Watanabe, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

MEDLINE 22354683

PUBMED 12466851

COMMENT
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FEATURES
Location/Qualifiers
1..350
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F83004F01"
/cvs_type="activated spleen"
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ORIGIN
Alignment Scores:
Pred. No.: 2,076-26 Length: 350
Score: 294.00 Matches: 62
Percent Similarity: 65.49% Conservative: 12
Best Local Similarity: 54.87% Mismatches: 37
Query Match: 42.36% Gaps: 2
DB: 13

US-09-195-368-1_COPY_48_177 (1-130) x BY216375 (1-350)

QY 6 ThrAlaValGluProCysMetAlaLysPheGlyProLeuProSerIleTyrGlnMetAla 25

Db 10 ACTGCATCGAGTCTGATGATGTTAACTATCATCTCAATAATGACATAGCA 69

QY 26 SerSerGluProProCysValAsnIleValSerAspTyrPheLeuGlnIleGlnAsn 45

Db 70 TCTCCCAACTCTGACTGTGTATATCGACATCTATGGAGAGCGAATATCTCGAGT 129

QY 46 GlyLeuTyrLeuIleTyrGlyGlnValAlaPro--AsnAlaLeuTyr--AsnAspVal 63

Db 130 GGCACATTTTAAATTAATGAGGCAAGTCTCTGATAGAAATAATCAATAAGACAT 189

QY 64 AlaProPheGluValAlaGluTyrLysAsnIleGlnIleGlnIleGlnIleGlnIle 83

Db 190 GCCCCTTCGATGATCAATATTAATAAAGAAATGTCCTAACAACCTTAATGATAT 249

QY 84 SerIleIleGlnAsnValGlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeu 103

Db 250 TTCAAACTGCTGATATAGAGAGGAGGTTATAGCATGCTGGAGATTAATATATCTG 309

QY 104 IlePheAsnSerGluHisGlnValLeuLysAsnThr 116

Db 310 AAGTCAACTTAAGACCATTAATTAAGAACTAACA 348

RESULT 4
BY214208 348 bp mRNA linear EST 10-DEC-2002

LOCUS BY214208

DEFINITION BY214208 RIKEN full-length enriched, activated spleen Mus musculus

ACCESSION BY214208

VERSION BY214208.1 GI:26394920

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamana, K., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusle, V., Chochoia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongawa, A., Kurochik, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Malat, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perle, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshak-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Garmus, P., Hayatsu, N., Hirozane-Kishikawa, T., Komori, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Waki, J., Aizawa, K., Aizawa, T., Fukuoka, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E., and Hayashizaki, Y.

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Nature 420, 563-573 (2002)

22354683

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COMMENT

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Adenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

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FEATURES

source

1.348 Location/Qualifiers

organism="Mus musculus"

molecule="mRNA"

strain="NOD"

ORIGIN

Alignment Scores:

Pred. No. 1,1e-19 Length: 348

Score: 240.00 Matches: 60

Percent Similarity: 62.28 Conservative: 11

Best Local Similarity: 52.63 Mismatches: 40

Query Match: 34.58 Indels: 4

DB: 13 Gaps: 2

US-09-195-368-1_COPY_48_177 (1-130) x BY214208 (1-348)

6 TTTTAAATTTTCCCTTAAAGGAGGCTTTATGAACTGCTGAGATGATATATCT 308

103 uilepnearsergluhsglnvalleuysasnthr 116

309 GAATTCACCTTAAGACCATTCATGAAACCTAACCA 348

RESULT 5

BY326400

LOCUS

DEFINITION

musculus cDNA clone 1030036x2 5', mRNA sequence.

ACCESSION

BY326400

VERSION

BY326400.1 GI:26516959

KEYWORDS

Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 348)

Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamana, K., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusle, V., Chochoia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongawa, A., Kurochik, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Malat, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perle, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wyshak-Boris, A., Yanagisawa, M., Yang, I.,

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COMMENT

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FEATURES
SOURCE

1.334
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="L030036422"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:
Pred. No.: 5.25e-07 Length: 334
Score: 138.00 Matches: 28
Percent Similarity: 67.39% Conservative: 3
Best Local Similarity: 60.87% Mismatches: 15
Query Match: 19.88% Indels: 0
Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x BY326400 (1-334)

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Db 195 ACTGCCATCGAGCTCTGATGGTTAAGTTTAAGTCACTATCACTCAAAATGGCACAATGCA 254

Qy 26 SerSerGinupPropocysVala1a1nysValSerAspTrpYsleuGinulleuGlnasn 45
Db 255 TCTCCCAACCTCACTCTGTCTCAATACACACATCTGATGGAGCGTGAAGATATCTCAGAGT 314
Qy 46 G1yLeuYrleu1e1yYr 51
Db 315 GGACATATTAATCTAC 332

RESULT 6
LOCUS BY326606
DEFINITION Mus musculus cDNA clone L030037A06 5', mRNA sequence.
ACCESSION BY326606
VERSION BY326606.1 GI:26517167
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
1 (bases 1 to 328)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Otsu, N., Sato, R., Suzuki, H., Yamanka, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schönbach, C., Gajober, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, J. M., Kanapin, A., Matsuda, H., Batalov, D. S., Belsel, K. W., Blake, J. A., Brad, D., Brusa, V., Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guerinovich, S., Hirokawa, N., Jackson, I. D., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, F. A., Maglocz, D. R., Maltale, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pettea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sander, A., Schneider, C., Semp, C. A., Serou, M., Shimada, K., Sultana, R., Takanaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Walstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wysshaw-Sorbs, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakakume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
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COMMENT

Contact: Yoshihide Hayashizaki
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Location/Qualifiers

1. 328

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="L030037A06"

/cell_type="synovial fibroblasts"

/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:

Pred. No.:	1,2e-05	Length:	328
Score:	127.00	Matches:	26
Percent Similarity:	65.91%	Conservative:	15
Best Local Similarity:	59.09%	Mismatches:	3
Query Match:	18.30%	Indels:	0
DB:	13	Gaps:	0

US-09-195-368-1_COPY_48_177 (1-130) x BY326606 (1-328)

QY 6 ThralalysGluProCyMetAlalysPheGlyProLeuProSerLyTyrGlnMetAla 25

DB 195 ACTGCATCGAGTCTCGATGATGTTAACTTGAACATCATCTCAAAATGCGACATACA 254

QY 26 SerSerGluProProCyValAsnLysValSerAspTPLYsLeuGluLeuGlnAsn 45

DB 255 TCTCCCAACCTCACTGTGTGTAATTCGACATCTGATGGAGAGCTGAAGATCTGCAAGT 314

QY 46 GlyLeuTyrLeu 49

DB 315 GGCACATATTTA 326

RESULT 7

BY327839

DEFINITION BY327839 RIKEN full-length enriched, synovial fibroblasts Mus

LOCUS BY327839 RIKEN full-length enriched, synovial fibroblasts Mus

ACCESSION BY327839

VERSION BY327839.1 GI:26516410

KEYWORDS EST

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 324)

Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamataka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojodori, T., Baladrelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schiml, L. M., Kanapin, A., Matsuuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V., Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Fraser, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Guettlich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Karai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numa, K., Okido, T., Pavani, W. J., Pettes, G., Pessio, G., Petrovsky, N., Pillai, R., Pontius, J. V., Qi, D., Ramchandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavoian, M., Zhu, Y., Zimmer, A., Zimmler, P., Hayatsu, N., Hirozane-Kashikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

12466851

22354683

CONTACT Yoshitake Hayashizaki

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The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gscc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/

Aizawa, K., Akimura, T., Arakawa, T., Gaminet, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Kono, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numataki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers

1. 324

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="L030044D24"

/cell_type="synovial fibroblasts"

/clone_lib="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:

Pred. No.:	3.71e-05	Length:	324
------------	----------	---------	-----

Score: 123.00 Matches: 25
 Percent Similarity: 65.12% Conservative: 3
 Best Local Similarity: 58.14% Mismatches: 15
 Query Match: 17.72% Indels: 0
 DB: 13 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x BY327839 (1-324)

QY 6 ThrAlaIysGIuProCyMeAlaIysPheGIyProLeuProSerIysTrpGIuMeAla 25
 |||||
 DB 195 ACTGCCAATCGAGCTTCAGTTCGTAATGCACTATCATCTCTCAAAATGGACATGACA 254
 |||||
 QY 26 SerSerGIuProProCyValAsnIysValSerAspTrpIysLeuGIuIleuGIuAsn 45
 |||||
 DB 255 TCTCCCAACCTACTCTGTGTGAATACGACATCTGATGGAGCTGAAGATCGACAGCT 314
 |||||
 QY 46 GlyLeuTyr 48
 |||||
 DB 315 GGACATAT 323

RESULT 8
 CG977950 114 bp DNA linear GSS 15-DEC-2003
 LOCUS CH240_168J10.TV CHORI-240 Bos taurus genomic clone CH240_168J10,
 DEFINITION genomic survey sequence.
 ACCESSION CG977950
 VERSION CG977950.1 GI:3903729
 KEYWORDS GSS.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 114)
 Costa, J.N., Mora, M. and Caetano, A.R.
 Brazil's Contribution to End-Sequencing the Bovine BAC Library
 CHORI-240
 Unpublished (2003)
 JOURNAL Other GSSs: CH240_168J10.TV
 COMMENT Contact: Caetano AR
 Department of Biotechnology
 Embrapa Recursos Geneticos e Biotecnologia
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.
 02372- 70770-900 Brasil
 Tel.: 55 61 448 4778
 Fax: 55 61 340 3658
 Email: acaetano@cenargen.embrapa.br
 Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm).
 Bases shown have Phred quality value equal to or higher than 20.
 Bases with quality value below 20 were masked with 'N'.
 For BAC library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm).
 This work was undertaken as part of the International Bovine BAC
 Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e
 Biotecnologia with financing from Conselho Nacional de
 Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil
 Plate: 168 Row: J Column: 10
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 114.

FEATURES

Location/Qualifiers
 1..114
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="Bred: Hereford"
 /db_xref="taxon:9913"
 /clone="CH240_168J10"
 /sex="Male"
 /cell_type="B100d"
 /clone_lib="CHORI-240"

ORIGIN

Alignment Scores:
 Pred. No.: 4.34e-05 Length: 114
 Score: 117.00 Matches: 19
 Percent Similarity: 85.19% Conservative: 4
 Best Local Similarity: 70.37% Mismatches: 4
 Query Match: 16.86% Indels: 0
 DB: 29 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x CG977950 (1-114)

QY 16 GlyProLeuProSerIysTrpGIuMeAlaSerSerGIuProProCyValAsnIysVal 35
 |||||
 DB 81 GAGCATTACCTTCGTAATGGCAATGCTCTCTCTAGAGCTTCTGTATGAAATGACA 22
 |||||
 QY 36 SerAspTrpIysLeuGIuIle 42
 |||||
 DB 21 CCGTACTGGAGAGCTGAAGATA 1

RESULT 9
 BU294618 727 bp mRNA linear EST 27-NOV-2002
 LOCUS BU294618
 DEFINITION 603603621P1 CSEQHN55 Gallus gallus CDNA clone CSE758216 5', mRNA
 sequence.
 ACCESSION BU294618
 VERSION BU294618.1 GI:25744254
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianine; Gallus.
 1 (bases 1 to 727)
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.U.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 JOURNAL 22335534
 MEDLINE 12445392
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Location/Qualifiers
 1..727
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CSE758216"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQHN55"
 /note="Organ: kidney + adrenal; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer.
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS

ORIGIN

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Alignment Scores:

Pred. No.:	0.00517	Length:	727
Score:	110.00	Matches:	38
Percent Similarity:	48.03%	Conservative:	23
Best Local Similarity:	29.92%	Mismatches:	46
Query Match:	15.85%	Indels:	20
DB:	13	Gaps:	6

US-09-195-368-1_COPY_48_177 (1-130) x BU294618 (1-727)

```

QY 15 PheGlyProLeuProSerIleTyrGlnMetAlaSerSerGluProProCyValAlaSer 34
DB 184 TTCTCCCAAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCAACGACGAGCTTG 237
QY 35 ValSer-----AspTrrPylSerGluIleLeuGlnAngIleTyrTyrLeuIleTyrGly 52
DB 238 AATCTCTACCATGAGGAGGAGCTGAAGTGAAGAGAGAGAGGCTCTACTACATCTACCA 297
QY 53 GlnValAlaProAlaAlaSerIleTyrAspValAlaProPheGluValArgLeuTyr--- 71
DB 298 CAAGTCAGCTTGTGACACCAAGGCGGCTTCGGGCGCATTCACCCCTATATTTATTTG 357
QY 72 -----LysAsnLysAspMetIleGlnThrLeu 80
DB 358 TACCTCCCATGAGAGAGACCGGCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
QY 81 ThrAsnLysSerIleLeuGlnAngIleTyrGlyTyrGluLeuHisValGly 98
DB 418 AGGCTCTCTGTGAGTCCATGCTCAGTCCGAGGAGGCTGTCTCTGAGCTCGGAGGAGG 477
QY 99 AspThr-----IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAspThr 116
DB 478 GACATGCTTGTGTCAATGTGACGACCTCAACAGCAAGTGAAGCTCAACCTCGGCAACCC 537
QY 117 TyrTrrGlyIleIleLeuLeu 123
DB 538 TACTTGGCATGTTCAGCTG 558

RESULT 10
BU373331 731 bp mRNA linear EST 28-NOV-2002
LOCUS 603589056F1 GSEQCHN74 Gallus gallus cDNA clone CHESTS49p13 5', mRNA
DEFINITION
ACCESSION BU373331.1 GI:25881332
VERSION BU373331
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
AUTHORS Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22355534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(MUMST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
location/Qualifiers
1. 731
FEATURES
source

```

ORIGIN

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton line 151"
/db_xref="taxon:9031"
/clone="CHESTS49p13"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="GSEQCHN74"
/note="Organ: Kidney + adrenal, Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

Alignment Scores:

Pred. No.:	0.00522	Length:	721
Score:	110.00	Matches:	38
Percent Similarity:	48.03%	Conservative:	23
Best Local Similarity:	29.92%	Mismatches:	46
Query Match:	15.85%	Indels:	20
DB:	13	Gaps:	6

US-09-195-368-1_COPY_48_177 (1-130) x BU373331 (1-731)

```

QY 15 PheGlyProLeuProSerIleTyrGlnMetAlaSerSerGluProProCyValAlaSer 34
DB 186 TTCTCCCAAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCAACGACGAGCTTG 239
QY 35 ValSer-----AspTrrPylSerGluIleLeuGlnAngIleTyrTyrLeuIleTyrGly 52
DB 240 AATCTCTACCATGAGGAGGAGCTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 299
QY 53 GlnValAlaProAlaAlaSerIleTyrAspValAlaProPheGluValArgLeuTyr--- 71
DB 300 CAAGTCAGCTTGTGACACCAAGGCGGCTTCGGGCGCATTCACCCCTATATTTATTTG 359
QY 72 -----LysAsnLysAspMetIleGlnThrLeu 80
DB 360 TACCTCCCATGAGAGAGACCGGCTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
QY 81 ThrAsnLysSerIleLeuGlnAngIleTyrGlyTyrGluLeuHisValGly 98
DB 420 ACGGCTCTGTGAGTCCATGCTCAGTCCGAGGAGGCTGTCTGAGCTGGGAGAGGAG 479
QY 99 AspThr-----IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnAspThr 116
DB 480 GACATGCTTGTGTCAATGTGACGACCTCAACAGCAAGTGAAGCTCAACCTCGGCAACCC 539
QY 117 TyrTrrGlyIleIleLeuLeu 123
DB 540 TACTTGGCATGTTCAGCTG 560

RESULT 11
A1982044 638 bp mRNA linear EST 07-MAY-2001
LOCUS A1982044
DEFINITION pat.pK0072.c9 f chicken activated T cell cDNA Gallus gallus cDNA
clone pat.pK0072.c9.f 5' similar to CD40 ligand, mRNA sequence.
ACCESSION A1982044
VERSION A1982044.1 GI:5885072
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

```


DB 324 CCAAGTGTCTCATCTTACTGTTGGAAATATTAACCTAGTAACAGTCAAGTCAAGG 383
 QY Asn-----LysValser 36
 DB 334 AACCTTACTTCTGGAATATCCGAGAGGTTGGCAAACTCGAGAAACATTAATACCAT 443
 QY 37 AsPTpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGly-----52
 DB 444 AACGAAAGCTGGAATCTTACAAAGATGCTATTCTGTATATGCAAACTGTGCTTT 503
 QY 53 -----GlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValArgLeu 70
 DB 504 AGACACCATATACATTAAGAAAGAAAGAAAGAAAGAGGCT---CTGCACTTATGATG 560
 QY 71 Tyr-----LysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLys 85
 DB 561 TACATCTGTAAAGCAAGCAAGCAAGAGGCTTATGAACGCTTATGAAGGAGGAAA 620
 QY 86 Ilegln-----AsnValGlyGlyThr 92
 DB 621 ACTGCCATTGTGCAAAATTAATTCAGCTATCATTTTATCTGTATATTAAGAGGGGTT 680
 QY 93 TyrGluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeu 112
 DB 681 TTTAATATACATGCTGCTGATCAGATA---TTTATCCAGAGCTCTTATTAAGACTGTG 737
 QY 113 -----LysAsnAsnThrTyrTyrGly 119
 DB 738 GACCCAGCAAGAAAGCTACATATTTGGG 767
 RESULT 13
 BM232049/c 575 bp mRNA linear EST 07-NOV-2002
 LOCUS BM232049 Nori Satoh unpublished cDNA library, young adult Ciona
 DEFINITION intestinalis cDNA clone ciad101c12 5', mRNA sequence.
 ACCESSION BM232049
 VERSION BM232049.1 GI:24753614
 KEYWORDS EST.
 SOURCE Ciona intestinalis
 ORGANISM Ciona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Stolidae; Ciona.
 REFERENCE 1 (bases 1 to 575)
 AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.
 TITLE Expressed genes in Ciona intestinalis (2002c)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113
 Email: satoh@scidian.zool.kyoto-u.ac.jp.
 FEATURES
 source location/Qualifiers
 1..575
 /organism="Ciona intestinalis"
 /mol_type="mRNA"
 /db_xref="taxon:7719"
 /clone="ciad101c12"
 /tissue_type="whole animal"
 /dev_stage="young adult"
 /clone_1lb="Nori Satoh unpublished cDNA library, young adult"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.74 Length: 575
 Score: 85.00 Matches: 28
 Percent Similarity: 43.64% Conservative: 26
 Best Local Similarity: 25.45% Mismatches: 30
 Query Match: 12.25% Indels: 26
 DB: 13 Gaps: 5

US-09-195-368-1_copy_48_177 (1-130) x BM232049 (1-575)
 QY 40 LeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsn 59
 DB 515 ATCAAAATCTGGAGAGCGGACTTATCAATTTACGGCGAGTAACATCCGCGCAACA 456
 QY 60 TyrAsnAspValAlaPro-----PheGlnValArgLeuTyrLysAsn 73
 DB 455 AGAACACGCTGTGACCTTGAGATGACAGCAAGTGTGTTGAAATACGAGATGCGACAT 396
 QY 74 ---LysAspMetIleGlnThrLeuThr-----AsnLysSerLys 85
 DB 395 CMCOCGATTTATTGAACACCAACACACAGACCTTATGAGATCATTTTCAATATCAAG 336
 QY 86 IleglnAsn-----ValGlyGlyThrTyrGluLeuHis 96
 DB 335 GCCATGACACACACCTCCCTCCAGATATGTTATTTAGGTGCTTACAAAGATTACAC 276
 QY 97 ValGlyAspThrIleAspLeuIlePheAsnSer-----GlnHisGlnValLeuLys 113
 DB 275 GCCGGTCAAGTATTTTNGTGATGATGAGACACACCGAGATGCGAAGGTACGATGCAACG 216
 QY 114 AsnAsnThrTyrTyrGlyIleIleLeuLeu 123
 DB 215 ACCGAAATTAATCTTGCGCATTCCTGCTC 186
 RESULT 14
 CG463627 878 bp DNA linear GSS 17-SEP-2003
 LOCUS ZUAKH11TV 2M 3.0 4.0 KB Zea mays genomic clone ZMMPBa0070A21,
 DEFINITION genomic survey sequence.
 ACCESSION CG463627
 VERSION CG463627.1 GI:34848627
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 878)
 AUTHORS WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,D.A., Rohlfing,T.,
 Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
 TITLE Consortium for Maize Genomics
 JOURNAL Unpublished (2002)
 COMMENT Other GSSs: ZUAKH11TH
 Contact: Cathy WhiteJaw
 TIGR Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteJaw@tigr.org
 Seg primer: TF
 Class: sheared ends.
 FEATURES
 source location/Qualifiers
 1..878
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMMPBa0070A21"
 /clone_1lb="ZM 3.0 4.0 kb"
 /note="Vector: pBESK-1; Site_1: HincII, 3-4 kb 'unfiltered' genomic DNA library"

ORIGIN
 Alignment Scores:
 Pred. No.: 8.93 Length: 878
 Score: 85.00 Matches: 26
 Percent Similarity: 43.33% Conservative: 13
 Best Local Similarity: 28.89% Mismatches: 27
 Query Match: 12.25% Indels: 24
 DB: 29 Gaps: 3

US-09-195-368-1_COPY_48_177 (1-130) x CG463627 (1-878)

QY 12 MetAlaLysPheGlyPProLeuProSerLysTrpGlnMetAlaSerSerGluProProCys 31
 DB 655 CTAGGACCTTTGGACCA-----AAGGCAAAATATCAAGTAAGGACCTTAA 705
 QY 32 ValAenLysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrlleuIleTy 51
 DB 706 ACCAACATCTCTTCACTGATGGAAATTTGCAAGTTGATGAGTAATTTG---GCTTAC 762
 QY 52 GlyGlnValAlaProAlaAsnTyLysAspValAlaProPheGluValArgLeuTy 71
 DB 763 TTGCAAAAGACACCCCATTAACCATAT-----789
 QY 72 LysAenLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGly 91
 DB 790 -----ATGCTTAAGTGTGAATTCAGTGCATGGGCTCA 822
 QY 92 ThrTyrgLileuHisValGlyAspThrIle 101
 DB 823 ACTTTGGAGCTCTATATCTCTCAATTCATA 852

RESULT 15

BZ758026 814 bp DNA linear GSS 10-MAR-2003
 BZ758026
 LOCUS PUBK49TD ZM 0.6-1.0 kb zea mays genomic clone ZM87A149101,
 DEFINITION genomic survey sequence.

ACCESSION BZ758026
 VERSION BZ758026.1 GI:28911400

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 814)

WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J., and
 Bennerzen,J.

Maize Genomics Consortium
 Unpublished (2003)

Other_GSSs: PUBK49TB

COMMENT Other: Cathy WhiteLaw

TI8R 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whiteLaw@igf.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..814
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZM87A149101"
 /clone_lib="ZM 0.6-1.0 KB"
 /note="vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 cot selected genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.: 9.2 Length: 814
 Score: 84.50 Matches: 34
 Percent Similarity: 39.34% Conservative: 14
 Best Local Similarity: 27.87% Mismatches: 29
 Query Match: 12.18% Indels: 45
 DB: 28 Gaps: 6

US-09-195-368-1_COPY_48_177 (1-130) x BZ758026 (1-814)

QY 12 MetAlaLysPheGlyPProLeuProSerLysTrpGlnMetAlaSerSerGluProProCys 31
 DB 225 CTAGGACCTTTGGACCA-----AAGGCAAAATATCAAGTAAGGACCTTAA 275
 QY 32 ValAenLysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrlleuIleTy 51
 DB 276 ACCAACATCTCTTCACTGATGGAAATTTGCAAGTTGATGAGTAATTTG---GCTTAC 332
 QY 52 GlyGlnValAlaProAlaAsnTyLysAspValAlaProPheGluValArgLeuTy 71
 DB 333 ATGCAAAAGACACCCCATTAACCATAT-----359
 QY 72 LysAenLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGly 91
 DB 360 -----ATGCTTAAGTGTGAATTCAGTGCATGGGCTCA 392
 QY 92 ThrTyrgLileuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnVal 111
 DB 393 ACTTTGGAGCTCTATATCTCT-----CAATTTC 419
 QY 112 LeuLysAsn-----AspThr-----TyTrpGlyIleIle 121
 DB 420 ATTAAGAAATTTGCCCTAGGTCAACATCAAGTTATAGAGCTACTATAGGGCTTAAC 479
 QY 122 LeuLeu 123
 DB 480 TTGCTT 485

Search completed: April 7, 2004, 19:35:59
 Job time: 1791.77 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:55:16 ; Search time 1941.11 Seconds
(without alignments)
2902.773 Million cell updates/sec

Title: US-09-195-368-1_COPY_48_177

Sequence: 1 FLOLETAKEPCMAKFGPLPS.....VKNTYWGILLANPQIS 130

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	694	100.0	510	9 AF117713	AF117713 Homo sapi
2	694	100.0	534	9 AF125303	AF125303 Homo sapi
3	694	100.0	1849	6 AR092586	AR092586 Sequence
4	694	100.0	1849	6 BD268764	BD268764 Human end
5	694	100.0	1849	6 AR214043	AR214043 Sequence
6	694	100.0	1849	6 AR282586	AR282586 Sequence
7	694	100.0	1964	6 AX074393	AX074393 Sequence
8	694	100.0	1964	6 AX077015	AX077015 Sequence
9	694	100.0	1964	6 AX080755	AX080755 Sequence
10	694	100.0	1964	6 AX150805	AX150805 Sequence
11	694	100.0	1964	6 AX391258	AX391258 Sequence
12	694	100.0	1964	6 BD085993	BD085993 Tumor nec
13	694	100.0	1964	6 BD124038	BD124038 Novel tum
14	694	100.0	1964	6 BD124046	BD124046 Novel tum
15	694	100.0	1964	6 AY358868	AY358868 Homo sapi
16	628	90.5	163136	9 HS15D23	AL031599 Human DNA
17	348	50.1	568	10 AY234223	AY234223 Mus muscu
18	348	50.1	1261	10 MMUS577580	AJ577580 Mus muscu
19	348	50.1	2066	10 MMUS77579	AJ577579 Mus muscu
20	344	49.6	522	10 AY267900	AJ267900 Mus muscu
21	342	49.3	522	10 AY359852	AY359852 Mus muscu
22	342	49.3	528	10 AY320040	AY320040 Mus muscu
23	325	46.8	228107	2 AC109057	AC109057 Rattus no
24	315	45.4	116159	2 AC117819	AC117819 Mus muscu
25	108.5	15.6	1892	5 GGA243435	AJ243435 Gallus ga
26	91	13.1	183800	2 EX628345	EX628345 Dario rer
27	91	13.1	197642	2 EX530057	EX530057 Dario rer
28	90	13.0	187859	2 BX323804	BX323804 Dario rer
29	90	13.0	193788	2 BX323559	BX323559 Dario rer
30	89	12.8	225126	2 AC138679	AC138679 Mus muscu
31	88	12.7	183818	5 BX649257	BX649257 Zebrafish
32	87	12.5	136581	9 AC008459	AC008459 Homo sapi
33	87	12.5	137324	9 AC018459	AC018459 Homo sapi
34	87	12.5	141591	9 AC079467	AC079467 Homo sapi
35	87	12.5	157122	9 AC079015	AC079015 Homo sapi
36	87	12.5	162162	9 AC012432	AC012432 Homo sapi
37	87	12.5	162705	9 AC099493	AC099493 Homo sapi
38	87	12.5	174086	2 AC110010	AC110010 Homo sapi
39	87	12.5	196922	2 BX470115	BX470115 Dario rer
40	87	12.5	199215	2 AC024422	AC024422 Homo sapi
41	86.5	12.5	183751	3 AC116551	AC116551 Dictyoste
42	86	12.4	183797	3 AC022400	AC022400 Homo sapi
43	86	12.4	196218	2 AC037447	AC037447 Homo sapi
44	86	12.4	207120	2 AL844520	AL844520 Homo sapi
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RESULT 1

ALIGNMENTS

LOCUS	AF117713	510 bp	mRNA	linear	PRI 09-MAR-1999
DEFINITION	Homo sapiens ATR ligand (TL6) mRNA, complete cds.				
ACCESSION	AF117713				
VERSION	AF117713.1	GI:4378801			
KEYWORDS					
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Kwon,B., Yu,K.Y., Ni,J., Yu,G.L., Jang,I.K., Kim,Y.T., Xing,L., Liu,D., Wang,S.X. and Kwon,B.S.				
TITLE	Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand				
JOURNAL	J. Biol. Chem. 274 (10), 6056-6061 (1999)				
MEDLINE	99156876				
PubMed	10037686				
REFERENCE	2 (bases 1 to 510)				
AUTHORS	Kwon,B., Yu,K.Y., Ni,J. and Kwon,B.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-JAN-1999) Micro. & Immunol., Indiana University, 635 Barnhall Dr., Indianapolis, IN 46202, USA				
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Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DA:	9	Gaps:	0		
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118 TTTCCTCAATGAGAGCTGCTAAAGAGCCCTGTAAGGCAATGCGCTTGGACATTACCTCA 177					
21 LysTrpGlnMetAlaSerSerGluProProCysValAsnIysValSerAspTrpIysLeu 40					
178 AATGCGCAAAATGSCATCTTCTGACACTCTTCGCGTAATPAAGTGCTGCTGCAAGCTG 237					
41 GlnIleLeuGlnAsnGlyLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60					
238 GAGATACCTTCAGAGAGCTTAATATTTAATTAAGGCAAGTGGCTCCCAATGCAAACTAC 297					
61 AsnAspValAlaProPheGlnValArgLeuIleuIleuIleuIleuIleuIleuIleuIleu 80					
298 AATGATGTAAGCTCTTTGAGGCGCGCTGTATAAACCAAGACATGATCAAACTCTA 357					
81 ThrAsnIysSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 100					
358 ACAAAACAATCTAAATCAAAATGAGAGGACCTTAAGAAATGATGTGGGACAC 417					

OY	101	ILASPLENILEPHEKSNSTRGJUHSGINVALEULEYASNASHNRHYRTPGJYLIE	120
Db	418	ATMACCTGATTTCACACTGTAGGCATCAGGTTCTTAAAAATAATACCTAGCGGGTATC	477
OY	121	IIEUDENUALAANPROGINPHELIESER	130
Db	478	ATTTACTGGCAATCCCATTCATCTCC	507
RESULT 2			
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LOCUS		Homo sapiens glucocorticoid-induced TNFR-related protein ligand	
DEFINITION		(TNFSF18) mRNA, complete cds.	
ACCESSION		AF125303	
VERSION		AF125303.1	GI:4558500
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE		1 (bases 1 to 534)	
JOURNAL		Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,	
REFERENCE		Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,	
AUTHORS		Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.	
TITLE		Identification of a new member of the tumor necrosis factor family	
JOURNAL		and its receptor, a human ortholog of mouse GITR	
REFERENCE		Curr. Biol. (1999) In press	
AUTHORS		2 (bases 1 to 534)	
TITLE		Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,	
JOURNAL		Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,	
REFERENCE		Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J. and Ashkenazi,A.	
AUTHORS		Direct Submission	
TITLE		Submitted (01-FEB-1999) Molecular Oncology, Genentech, 1 DNA Way,	
JOURNAL		South San Francisco, CA 94080, USA	
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Pred. No.:	2,58e-69	Length:	534
Score:	694.00	Matches:	130
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QY 21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
Db 202 AATGGCAATGGCACTTCTGAACTCTTGCGTAATAGGTGTCTGACGAAAGCTG 261
QY 41 GlnLleuGlnAsnGlyLeuLysLeuLysGlyGlnValAlaProAsnAlaAsnTrp 60
Db 262 GAGATCTTCAGATGGCTTATTTAATTATGGCAAGTGGCTCCCAATGCAACAC 321
QY 61 AsnAspValAlaProPheGlnValArgLeuLysValAsnLysAspMetLleGlnTrpLeu 80
Db 322 AATGATGATGACTCTTTTGAAGTGGCGCTGTATMAAACAAGACATGATACAACTCA 381
QY 81 ThrAsnLysSerLysLleGlnAsnValGlyGlyThrTrpGlnLeuHisValGlyAspThr 100
Db 382 ACAACCAATCTAAATCCAAATGTAGAGGAGACTTATGAATTGATGTGGGACAC 441
QY 101 IleAspLleuLlePheAsnSerGlnHisGlnValLleuLysAsnAsnThrTrpTrpGlyLle 120
Db 442 ATGAGCTTGATTTCACTCTGAGCATCAGGTTCTTAAATAATATCATCTGGGGATC 501
QY 121 IleLeuLleuAlaAsnProGlnPheLleSer 130
Db 502 ATTTACTACCAATCCCAATCATCTCC 531
RESULT 3
AR092586 1849 bp DNA linear PAT 08-SEP-2000
LOCUS AR092586
DEFINITION Sequence 1 from patent US 5998171.
ACCESSION AR092586
VERSION AR092586.1 GI:10019339
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Yu, G.-L., Ni, J., and Rosen, C.A.
TITLE Polynucleotides encoding human endokine alpha
JOURNAL Patent: US 5998171-A 1 07-DEC-1999;
FEATURES
Location/Qualifiers
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QY 1 PheLeuGlnLeuGlnThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
Db 170 TTCTCCAAATTAGAGCTGCTAGAGACCTGTATGCTAGATTGGAACCATTAACCTCA 229
QY 21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
Db 230 AATGGCAATGGCACTTCTGAACTCTTGCGTAATAGGTGTCTGACGAAAGCTG 289
QY 41 GlnLleuGlnAsnGlyLeuLysLeuLysGlyGlnValAlaProAsnAlaAsnTrp 60
Db 290 GAGATCTTCAGATGGCTTATTTAATTATGGCAAGTGGCTCCCAATGCAACAC 349
QY 61 AsnAspValAlaProPheGlnValArgLeuLysValAsnLysAspMetLleGlnTrpLeu 80
Db 350 AATGATGATGACTCTTTTGAAGTGGCGCTGTATMAAACAAGACATGATACAACTCA 409
QY 81 ThrAsnLysSerLysLleGlnAsnValGlyGlyThrTrpGlnLeuHisValGlyAspThr 100
Db 410 ACAACCAATCTAAATCCCAATGTAGAGGAGACTTATGAATTGATGTGGGACAC 469

QY 101 IleAspLleuLlePheAsnSerGlnHisGlnValLleuLysAsnAsnThrTrpTrpGlyLle 120
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QY 121 IleLeuLleuAlaAsnProGlnPheLleSer 130
Db 530 ATTTACTACCAATCCCAATCATCTCC 559
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BD268764 1849 bp DNA linear PAT 17-JUL-2003
LOCUS BD268764
DEFINITION Human endokine alpha and methods of use.
ACCESSION BD268764
VERSION BD268764.1 GI:33078532
KEYWORDS JP 2002537769-A/1.
SOURCE JP 2002537769-A/1.
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Yu, G.-L., Ni, J., and Rosen, C.A.
TITLE Human endokine alpha and methods of use
JOURNAL Patent: JP 2002537769-A 1 12-NOV-2002;
HUMAN GENOME SCIENCES INC
OS Artificial Sequence
COMMENT PN JP 2002537769-A/1
PD 12-NOV-2002
PF 25-FEB-2000 JP 2000601183
PR 26-FEB-1999 US 60/122099, 28-MAY-1999 US 60/136788 PI
GUO LIANG YU, JIAN NI, CRAIG A ROSEN
PC C12N15/09, A61K38/22, A61K39/395, A61K39/395, A61K45/00, A61P1/00,
PC A61P1/16, A61P3/02, A61P3/04, A61P3/06, A61P3/08, A61P3/10, A61P11/06 PC
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PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12N15/00, C12N5/
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CC endokine alpha protein
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Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-195-368-1_COPY_48_177 (1-130) x BD268764 (1-1849)
QY 1 PheLeuGlnLeuGlnThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
Db 170 TTCTCCAAATTAGAGCTGCTAGAGACCTGTATGCTAGATTGGAACCATTAACCTCA 229
QY 21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTrpLysLeu 40
Db 230 AATGGCAATGGCACTTCTGAACTCTTGCGTAATAGGTGTCTGACGAAAGCTG 289
QY 41 GlnLleuGlnAsnGlyLeuLysLeuLysGlyGlnValAlaProAsnAlaAsnTrp 60
Db 290 GAGATCTTCAGATGGCTTATTTAATTATGGCAAGTGGCTCCCAATGCAACAC 349

QY 61 AsnAspValAlaProPheGluValAlaArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
 Db 350 AATATATGATCTCTTTTGGAGTGGCTGTATATAAACAAGACATGATACCAACTCTA 409
 QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluPheHisValGlyAspThr 100
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 QY 101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnSerThrTyrTrpGlyIle 120
 Db 470 ATAGACTTGATATCACTCGAGCATCAGGTTCTAAAAAATATACCTACCTGGGATAC 529
 QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
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RESULT 5

AR214043 1849 bp mRNA linear PAT 25-SEP-2002
 LOCUS AR214043
 DEFINITION Sequence 1 from patent US 6406867.
 ACCESSION AR214043
 VERSION AR214043.1 GI:23311480
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 1849)
 AUTHORS Yu, G.-L., Ni, J. and Rosen, C. A.
 TITLE Antibody to human endokine alpha and methods of use
 JOURNAL Patent: US 6406867-A 1 18-JUN-2002;
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ORIGIN

Alignment Scores:
 Pred. No.: 1,11e-68 Length: 1849
 Score: 694.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 100.00% Indels: 0
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US-09-195-368-1_COPY_48_177 (1-130) x AR214043 (1-1849)

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 Db 290 GAGATACCTTCGATAGCTTATATTATTAATTATGCGCAAGTGGTCCCAATGCAAACTAC 349
 QY 61 AsnAspValAlaProPheGluValAlaArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
 Db 350 AATGATGAGCTCTTTTGGAGTGGCTGTATATAAACAAGACATGATACCAACTCTA 409
 QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluPheHisValGlyAspThr 100
 Db 410 ACAACCAATCTAAATCCAAATGTAGAGGACCTTATTAATTCATGTGGGACACC 469
 QY 101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnSerThrTyrTrpGlyIle 120
 Db 470 ATAGACTTGATATCACTCGAGCATCAGGTTCTAAAAAATATACCTACCTGGGATAC 529
 QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
 Db 530 ATTTACTAGCAATCCCAATTCATCTCC 559

Db 530 ATTTACTAGCAATCCCAATTCATCTCC 559

RESULT 6
 AR282586 1849 bp mRNA linear PAT 10-APR-2003
 LOCUS AR282586
 DEFINITION Sequence 1 from patent US 6521742.
 ACCESSION AR282586
 VERSION AR282586.1 GI:29719155
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 1849)
 AUTHORS Yu, G.-L., Ni, J. and Rosen, C. A.
 TITLE Human endokine alpha
 JOURNAL Patent: US 6521742-A 1 18-FEB-2003;
 FEATURES
 source Location/Qualifiers
 1..1849
 /organism="unknown"
 /mol_type="mRNA"

ORIGIN

Alignment Scores:
 Pred. No.: 1,11e-68 Length: 1849
 Score: 694.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AR282586 (1-1849)

QY 1 PheLeuGlnLeuGlnThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSer 20
 Db 170 TTTCCTCCAAATTAGAGACTGTAGAGAGCCCTGTATAGCTTAAGTTGGACCATTAACCTCA 229
 QY 21 LysTrpGlnMetAlaSerSerGluProCysValAsnLysValSerAspTrpLysLeu 40
 Db 230 AAAAGGCAAAATGGCATCTTCTGAACCTTCCTGCGTAAATAGAGGTGTGACTGGAAGCTG 289
 QY 41 GluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyr 60
 Db 290 GAGATACCTTCGATAGCTTATATTATTAATTATGCGCAAGTGGTCCCAATGCAAACTAC 349
 QY 61 AsnAspValAlaProPheGluValAlaArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
 Db 350 AATGATGAGCTCTTTTGGAGTGGCTGTATATAAACAAGACATGATACCAACTCTA 409
 QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrGluPheHisValGlyAspThr 100
 Db 410 ACAACCAATCTAAATCCAAATGTAGAGGACCTTATTAATTCATGTGGGACACC 469
 QY 101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnSerThrTyrTrpGlyIle 120
 Db 470 ATAGACTTGATATCACTCGAGCATCAGGTTCTAAAAAATATACCTACCTGGGATAC 529
 QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
 Db 530 ATTTACTAGCAATCCCAATTCATCTCC 559

RESULT 7
 AX074393 1964 bp DNA linear PAT 06-FEB-2001
 LOCUS AX074393
 DEFINITION Sequence 13 from Patent WO0103720.
 ACCESSION AX074393
 VERSION AX074393.1 GI:12710533
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCES
 1 Williams, P.M. and Gerritsen, M.E.

TITLE
JOURNAL
Genentech, Inc. (US)
Patent: WO 0103720-A 13 18-JAN-2001;

FEATURES
source
1. 1964
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1.19e-68 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AX074393 (1-1964)

QY 1 PheLeuGlnLeuGluThralAlaLysGluProCyMeAlaLysPheGlyProLeuProSer 20
Db 162 TTCTCCAAATTAGAGCTGCTAGAGCCCTGTATGGCTAAGTTGACCATTAACCTCA 221
QY 21 LysTrpGlnMetAlaSerSerGluProProCyValAsnLysValSerAspTrpLysLeu 40
Db 222 AATGGCAATGGCATCTTCTGAACTCTGCGGTGAATAGGTGTCTAGCTGAAGCTG 281
QY 41 GluLeuGlnAsnGlyLeuTyLeuLeuTyGlyGlnValAlaProAsnAlaAsnTy 60
Db 282 GAGATCTTGAGATGGCTTATATTATTTATGCGCAAGTGGCTCCCAATGCAACTAC 341
QY 61 AsnAspValAlaProPheGluValArgLeuTyLysAsnLysAspMetIleGlnThrLeu 80
Db 342 AATGATGTAGCTCTCTTTGAGTGGCGGCTGTATTAACCAAGACATGATCAACTCA 401
QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyGlnLeuHisValGlyAspThr 100
Db 402 ACAACCAATCTTAATCCAAATGTAGAGGACCTTATATGATTCATGTGGGACACC 461
QY 101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnThrTyTrpGlyIle 120
Db 462 ATGACTGTGATATCACTGAGACATCAGGTCTTAATAAATATACATCTGGGTATC 521
QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
Db 522 ATTCTACTAGCAATCCCAATTCATCTCC 551

RESULT 8
AX077015 1964 bp DNA linear PAT 22-FEB-2001
LOCUS
DEFINITION Sequence 3 from Patent WO0105972.
ACCESSION AX077015
VERSION AX077015.1 GI:13121653
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,
Tunna, D., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of immune related
diseases
Patent: WO 0105972-A 3 25-JAN-2001;

TITLE
JOURNAL
Genentech, Inc. (US)
Patent: WO 0105972-A 3 25-JAN-2001;
FEATURES
source
1. 1964
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1.19e-68 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AX077015 (1-1964)

QY 1 PheLeuGlnLeuGluThralAlaLysGluProCyMeAlaLysPheGlyProLeuProSer 20
Db 162 TTCTCCAAATTAGAGCTGCTAGAGCCCTGTATGGCTAAGTTGACCATTAACCTCA 221
QY 21 LysTrpGlnMetAlaSerSerGluProProCyValAsnLysValSerAspTrpLysLeu 40
Db 222 AATGGCAATGGCATCTTCTGAACTCTGCGGTGAATAGGTGTCTAGCTGAAGCTG 281
QY 41 GluLeuGlnAsnGlyLeuTyLeuLeuTyGlyGlnValAlaProAsnAlaAsnTy 60
Db 282 GAGATCTTGAGATGGCTTATATTATTTATGCGCAAGTGGCTCCCAATGCAACTAC 341
QY 61 AsnAspValAlaProPheGluValArgLeuTyLysAsnLysAspMetIleGlnThrLeu 80
Db 342 AATGATGTAGCTCTCTTTGAGTGGCGGCTGTATTAACCAAGACATGATCAACTCA 401
QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyGlnLeuHisValGlyAspThr 100
Db 402 ACAACCAATCTTAATCCAAATGTAGAGGACCTTATATGATTCATGTGGGACACC 461
QY 101 IleAspLeuIlePheAsnSerGluHisGlnValLeuLysAsnThrTyTrpGlyIle 120
Db 462 ATGACTGTGATATCACTGAGACATCAGGTCTTAATAAATATACATCTGGGTATC 521
QY 121 IleLeuLeuAlaAsnProGlnPheIleSer 130
Db 522 ATTCTACTAGCAATCCCAATTCATCTCC 551

RESULT 9
AX080755 1964 bp DNA linear PAT 27-FEB-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0109327.
ACCESSION AX080755
VERSION AX080755.1 GI:13169735
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
1 Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J., Gurney, A.L.,
Klavins, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,
Watanabe, C.K. and Wood, W.I.
Method of preventing the injury or death of retinal cells and
treating ocular diseases
Patent: WO 0109327-A 1 08-FEB-2001;

TITLE
JOURNAL
Genentech, Inc. (US)
Patent: WO 0109327-A 1 08-FEB-2001;
FEATURES
source
1. 1964
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.19e-68 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AX080755 (1-1964)

QY 1 PheleuglnleuglnThralalysglupProCyseMetalaalyPhegIyProleuProser 20
 Db 162 TTTCTCCATTGAGACTGCTAAGAGCCCTGTATGGCTTAAGTTGGACATTACCTCA 221
 QY 21 LysTIPGlnMetalaaserseglupProCyseValasnllyValseraspTIPlyseu 40
 Db 222 AAATGGCAATGGCACTCTTCTGAACCTCCTGGTAAATPAAGGTGTCTACTGGAAGCTG 281
 QY 41 GluIleleuglnasnglyleuTyrlleuIleTyrglyGlnValaIaProasnlIasnyr 60
 Db 282 GAGATCTTCAGAAATGGCTTATTTATTTATTTAGGCCAATGGCTCCCAATCAAACTAC 341
 QY 61 AsnaspValaIaProPhegluValaIargleuTyrllyAsnlyAspMetIleglnThrlleu 80
 Db 342 AATGATGTAGCTCCTTTTGAGTGCGGCTGTATAAAAACAAAGACATGATCAAACTCTA 401
 QY 81 ThrAsnlyseerlyseIleglnasnlValaIglyTyrlThyrglyleuHlsValaIyAspThr 100
 Db 402 ACAACAAATCTAAATCCAAATGTAGAGGACCTTATGATTCATGTGGGACAC 461
 QY 101 IleAspIleuIlePheasensegluHlsGlnValleuIyAsnAsnThrTyrlTPGlyIle 120
 Db 462 ATGACTTGATATTCACACTCTGAGCATCAGGTTCTAAAAATATACATACCTGGGTATC 521
 QY 121 IleleuIleuIaAsnProglInPheIleSer 130
 Db 522 ATTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 10
 AX150805 1964 bp DNA linear PAT 22-JUN-2001
 LOCUS AX150805
 DEFINITION Sequence 1 from Patent WO0140464.
 ACCESSION AX150805
 VERSION AX150805.1 GI:14533039

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Ashkenazi, A.J., Baker, K.P., Ferrara, N., Godowski, P.J., Guney, A.L., Hillan, K.J., Mark, M.R., Masters, S.A., Paoni, N.F., Pittel, R.M. and Wood, W.I.
 TITLE Interleukin-1-receptor associated kinase-3 (Irak3) and its use in promotion or inhibition of angiogenesis and cardiovascularization
 JOURNAL Patent: WO 0140464-A 1 07-JUN-2001;

FEATURES
 source Location/Qualifiers
 1..1964
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,196-68 Length: 1964
 Score: 694.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AX150805 (1-1964)
 QY 1 PheleuglnleuglnThralalysglupProCyseMetalaalyPhegIyProleuProser 20
 Db 162 TTTCTCCATTGAGACTGCTAAGAGCCCTGTATGGCTTAAGTTGGACATTACCTCA 221
 QY 21 LysTIPGlnMetalaaserseglupProCyseValasnllyValseraspTIPlyseu 40

QY 41 GluIleleuglnasnglyleuTyrlleuIleTyrglyGlnValaIaProasnlIasnyr 60
 Db 282 GAGATCTTCAGAAATGGCTTATTTATTTATTTAGGCCAATGGCTCCCAATCAAACTAC 341
 QY 61 AsnaspValaIaProPhegluValaIargleuTyrllyAsnlyAspMetIleglnThrlleu 80
 Db 342 AATGATGTAGCTCCTTTTGAGTGCGGCTGTATAAAAACAAAGACATGATCAAACTCTA 401

Db 222 AAATGGCAATGGCACTCTTCTGAACCTCCTGGTAAATPAAGGTGTCTACTGGAAGCTG 281

QY 41 GluIleleuglnasnglyleuTyrlleuIleTyrglyGlnValaIaProasnlIasnyr 60
 Db 282 GAGATCTTCAGAAATGGCTTATTTATTTATTTAGGCCAATGGCTCCCAATCAAACTAC 341

QY 61 AsnaspValaIaProPhegluValaIargleuTyrllyAsnlyAspMetIleglnThrlleu 80
 Db 342 AATGATGTAGCTCCTTTTGAGTGCGGCTGTATAAAAACAAAGACATGATCAAACTCTA 401

QY 81 ThrAsnlyseerlyseIleglnasnlValaIglyTyrlThyrglyleuHlsValaIyAspThr 100
 Db 402 ACAACAAATCTAAATCCAAATGTAGAGGACCTTATGATTCATGTGGGACAC 461

QY 101 IleAspIleuIlePheasensegluHlsGlnValleuIyAsnAsnThrTyrlTPGlyIle 120
 Db 462 ATGACTTGATATTCACACTCTGAGCATCAGGTTCTAAAAATATACATACCTGGGTATC 521

QY 121 IleleuIleuIaAsnProglInPheIleSer 130
 Db 522 ATTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 11
 AX391258 1964 bp DNA linear PAT 23-MAR-2002
 LOCUS AX391258
 DEFINITION Sequence 1 from Patent WO0073445.
 ACCESSION AX391258
 VERSION AX391258.1 GI:19699932

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., Goddard, A., Godowski, P.J., Guney, A.L., Kuo, S.S., Mark, M.R., Masters, S.A., Pittel, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni, N.F. and Watanabe, C.K.
 TITLE Promotion or inhibition of angiogenesis and cardiovascularization
 JOURNAL Patent: WO 0073445-A 1 07-DEC-2000;

FEATURES
 source Location/Qualifiers
 1..1964
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 1,196-68 Length: 1964
 Score: 694.00 Matches: 130
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-195-368-1_COPY_48_177 (1-130) x AX391258 (1-1964)
 QY 1 PheleuglnleuglnThralalysglupProCyseMetalaalyPhegIyProleuProser 20
 Db 162 TTTCTCCATTGAGACTGCTAAGAGCCCTGTATGGCTTAAGTTGGACATTACCTCA 221
 QY 21 LysTIPGlnMetalaaserseglupProCyseValasnllyValseraspTIPlyseu 40
 Db 222 AAATGGCAATGGCACTCTTCTGAACCTCCTGGTAAATPAAGGTGTCTACTGGAAGCTG 281

QY 41 GluIleleuglnasnglyleuTyrlleuIleTyrglyGlnValaIaProasnlIasnyr 60
 Db 282 GAGATCTTCAGAAATGGCTTATTTATTTATTTAGGCCAATGGCTCCCAATCAAACTAC 341

QY 61 AsnaspValaIaProPhegluValaIargleuTyrllyAsnlyAspMetIleglnThrlleu 80
 Db 342 AATGATGTAGCTCCTTTTGAGTGCGGCTGTATAAAAACAAAGACATGATCAAACTCTA 401

QY 81 ThrAsnlyseerlyseIleglnasnlValaIglyTyrlThyrglyleuHlsValaIyAspThr 100
 Db 402 ACAACAAATCTAAATCCAAATGTAGAGGACCTTATGATTCATGTGGGACAC 461
 QY 101 IleAspIleuIlePheasensegluHlsGlnValleuIyAsnAsnThrTyrlTPGlyIle 120
 Db 462 ATGACTTGATATTCACACTCTGAGCATCAGGTTCTAAAAATATACATACCTGGGTATC 521
 QY 121 IleleuIleuIaAsnProglInPheIleSer 130
 Db 522 ATTTACTAGCAAAATCCCAATTCATCTCC 551

QY 81 Thrasnlyserlyslleglnsnvalglylthrttygluleuh:valgiaspthr 100
DB 402 ACAACCAATCTAAATTCAAAATGTAGAGGACCTTGAATTGCACTTGGGACACC 461
QY 101 lileaspleuilepheasnsergiuhisglnvalleuylasasnthrtyttrpglytle 120
DB 462 ATAGACTTGATATTCAGCTGAGCATCAGTTCTTAAAAATAATACATACGAGGATAC 521
QY 121 lileuleuualasnproginphelieser 130
DB 522 ATTTACTAGCAAAATCCCAATTCATCTCC 551
RESULT 12
BD085993 1964 bp DNA linear PAT 27-AUG-2002
LOCUS Tumor necrosis factor homolog DNA19355 polypeptide.
DEFINITION BD085993
ACCESSION BD085993.1 GI:22631603
VERSION JP 2001523459-A/1.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1964)
AUTHORS Ashkenazi, A.J., Gurney, A.L., Marsters, S.A., Robert, Pitti,
Baker, K.P., Godowski, P.J. and Mark, M.R.
Tumor necrosis factor homolog DNA19355 polypeptide
Patent: JP 2001523459-A 1 27-NOV-2001;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2001523459-A/1
PD 27-NOV-2001 JP 2000521199
PF 18-NOV-1998 US 60/065635,12-DEC-1997 US 60/065661 PI
AVI J ASHKENAZI, AUSTIN L GURNEY, SCOT A MARSTERS, ROBERT PI
PITTI, KEVIN P BAKER,
PI PAUL J GODOWSKI, MELANIE R MARK
PC C12N15/09, A61K38/00, A61P35/00, C07K14/525, C07K16/24, C07K19/00,
PC C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, C12P21/08, C12P21/02, C12R1/19,
PC C12P21/02, C12R1/91, C12N15/00, A61K37/02, C12N5/00 CC Tumor
necrosis factor homolog DNA19355 polypeptide FH Key
Location/Qualifiers
FT source 1..1964
/organism="Homo sapiens (human)".
FEATURES
source Location/Qualifiers
1..1964
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.19e-68 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-195-368-1_COPY_48_177 (1-130) x BD085993 (1-1964)
QY 1 Phleuglnleuglnthralalygsluprocymetalaalyspdehlyproleuprosar 20
DB 162 TTTCCTCAATTAGAGACTGCTAGAGAGCCCTGTATGCTTGTGACCATTAACCTCA 221
QY 21 llyttrglnmetlaserasergiupropocymetalaalyspdehlyproleuprosar 40
DB 222 AAATGGCAAAAGGACATCTTCGAACTCCCTGGGATGATAGAGTGTCTGACGGAAGCTG 281
QY 41 Gluleleuglnsnnglyleuylthrttygluleuh:valgiaspthr 60

DB 282 GAGATACCTCAGAAATGCTTAATTTAATTTATGCCCAAGTGCTCCCAATGCAACTAC 341
QY 61 Asnaspvalalaprohegnluvalargleuyltlyslasnllyaspnellieglnthleu 80
DB 342 AATGATGATGCTCTTTTGGGTGGCGGTGTATAAAAACAAGACATGATACAACTCTA 401
QY 81 Thrasnlyserlyslleglnsnvalglylthrttygluleuh:valgiaspthr 100
DB 402 ACAACCAATCTAAATTCAAAATGTAGAGGACCTTGAATTGCACTTGGGACACC 461
QY 101 lileaspleuilepheasnsergiuhisglnvalleuylasasnthrtyttrpglytle 120
DB 462 ATAGACTTGATATTCAGCTGAGCATCAGTTCTTAAAAATAATACATACGAGGATAC 521
QY 121 lileuleuualasnproginphelieser 130
DB 522 ATTTACTAGCAAAATCCCAATTCATCTCC 551
RESULT 13
BD124038 1964 bp DNA linear PAT 18-SEP-2002
LOCUS Novel tumor necrosis factor receptor homolog and nucleic acid
DEFINITION BD124038
ACCESSION BD124038.1 GI:23218983
VERSION JP 2002502607-A/14.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1964)
AUTHORS Ashkenazi, A.J., Gurney, A.L., Marsters, S.A., Pitti, R.M., Wood, W.I.
and Goddard, A.
Novel tumor necrosis factor receptor homolog and nucleic acid
encoding the same
Patent: JP 2002502607-A 14 29-JUN-2002;
GENENTECH INC
COMMENT OS Homo sapiens (human)
PN JP 2002502607-A/14
PD 29-JUN-2002
PF 09-FEB-1998 JP 2000530610
PR 09-FEB-1998 US 60/074 087
PI AVI J ASHKENAZI, AUSTIN L GURNEY, SCOT A MARSTERS, ROBERT M
PITTI,
PI WILLIAM I WOOD, AUDLEY GODDARD
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61P29/00, A61P37/06,
PC A61P43/00,
PC C07K14/705, C07K16/28, C07K19/00, C12N1/19, C12N1/21, C12N5/10, PC
C12P21/02, C07K14/47, C12N15/00, A61K37/02, C12N5/00 CC Novel
tumor necrosis factor receptor homolog and nucleic acid CC
encoding the
CC same
FH Key
FT source 1..1964
/organism="Homo sapiens (human)".
FEATURES
source Location/Qualifiers
1..1964
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.19e-68 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-195-368-1_COPY_48_177 (1-130) x BD124038 (1-1964)

QY 1 Pheleuglnleuglnlthralalysgluprocysmelaalysphcglyproleuprosr 20
Db 162 TTTCTCCATTAGAGACTGCTAGAGAGCCCTGTATGGCTTAAGTTTGACCATTAACCTCA 221
QY 21 LysTrpGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTyrLysLeu 40
Db 222 AAATGGCAATGGCACTCTTGAACCTCTTGCGTGAATAGGTGTCTACTGAGAGCTG 281
QY 41 GluIleleuglnaanglyleuTyLeuIleTyGlyGlnValAlaProAsnAlaAsnTyr 60
Db 282 GAGATCTTCAGATGGCTTATATTATTTATTTATGCGCAATGGCTCCCAATGCAACTAC 341
QY 61 AsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMetIleGlnThrLeu 80
Db 342 AATGATGTACTCTCTTTTGAGTGGCGGTGTATATAAACAAGACATGATACCAACTCTA 401
QY 81 ThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyGlnLeuHisValGlyAspThr 100
Db 402 ACAACCAATCTAAATCCAAATGTAGAGGAGCTTATGCAATTCATGTGGGACAC 461
QY 101 IleAspLeuIlePheAsnSerGluHisGlnValleuLysAsnAsnThrTyrTrpGlyIle 120
Db 462 ATGACTGTGATTCACACTGTGAGCATCAGGTTCTATAAATAATACATACCTGGGATATC 521
QY 121 IleleuLeuAlaAsnProGlnPheIleSer 130
Db 522 ATTTTACTAGCAATCCCAATTCATCTCC 551

RESULT 14
BD124046/c 1964 bp DNA linear PAR 18-SEP-2002
LOCUS Novel tumor necrosis factor receptor homolog and nucleic acid
DEFINITION encoding the same.
ACCESSION BD124046.1 GI:23218991
VERSION UP 2002502607-A/22.
KEYWORDS Homo sapiens (human)
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ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1964)
AUTHORS Ashkenazi, A., Gurney, A.L., Marsters, S.A., Pitti, R.M., Wood, W.I.
and Goddard, A.
TITLE Novel tumor necrosis factor receptor homolog and nucleic acid
encoding the same
JOURNAL Patent: JP 2002502607-A 22 29-JAN-2002;
COMMENT GENENTECH INC
OS Homo sapiens (human)
PN JP 2002502607-A/22
PD 29-JAN-2002
PF 09-FEB-1999 JP 2000530610
PR 09-FEB-1998 US 60/074 087
PI AVI J ASHKENAZI, AUSTIN L GURNEY, SCOT A MARSTERS, ROBERT M
PITTI,
PC WILLIAM J WOOD, AUDLEY GODDARD
PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61P29/00, A61P37/06,
PC A61P43/00, A61K38/00, A61K39/395, A61K39/395, A61P29/00, A61P37/06,
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VERSION FL1_CDNA.
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SOURCE
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Homo sapiens (human)
REFERENCE 1 (bases 1 to 1964)
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,
Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B.,
Dowd, P., Eaton, D., Foster, J., Gilmaldi, C., Gu, Q., Hass, P.E.,
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Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z.,
Goddard, A., Wood, W.I., and Goddard, W.I.
TITLE The Secreted Protein Discovery Initiative (SPDI): a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975109
REFERENCE 2 (bases 1 to 1964)
AUTHORS Clark, H.F.
DIRECT SUBMISSION
SUBMITTED (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

Alignment Scores:
Pred. No.: 1.19e-68 Length: 1964
Score: 694.00 Matches: 130
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Job time: 1955.11 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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(without alignments)
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Title: US-09-195-368-1

Perfect score: 951

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Searched: 682709 seqs, 277475446 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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6	84.5	8.9	3666	4	US-09-107-532A-305
7	82.5	8.7	457	4	US-09-621-976-13182
8	80.5	8.5	21368	4	US-09-851-985-3
9	80	8.4	1219	3	US-09-230-380-10
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C 18	75.5	7.9	3420	3	US-09-039-859-8	Sequence 8, Appl 1
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C 20	75	7.9	1175	4	US-09-489-847-105	Sequence 105, App
C 21	74.5	7.8	699	3	US-08-998-416-717	Sequence 717, App
C 22	74.5	7.8	1720	4	US-09-227-357-139	Sequence 139, App
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ALIGNMENTS

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Sequence 1, Application US/08912227
Patent No. 5998171
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
TITLE OF INVENTION: Human Endokine Alpha
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,227
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,058
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0470001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1849 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 53..559
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Query Match: 100.00% Indels: 0
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; Sequence 1, Application US/09513584
; Patent No. 6406867
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; TITLE OF INVENTION: Human Endocrine Alpha and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX,
; ADDRESSEE: P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/513,584
FILING DATE: 25-FEB-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,058
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,227
FILING DATE: 15-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/122,099
FILING DATE: 26-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/136,788
FILING DATE: 28-MAY-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/345,790
FILING DATE: 01-JUL-1999
ATTORNEY/AGENT INFORMATION:
NAME: Steife, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488,0470005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 53..559
US-09-513-584-1

Alignment Scores:
Pred. No.: 6,54e-118 Length: 1849
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

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RESULT 3

US-09-345-790-1
 ; Sequence 1, Application US/09345790
 ; Patent No. 6521742

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
 APPLICANT: Ni, Jian
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: Human Endokine Alpha
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

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 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent-in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/345,790

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/912,227

ATTORNEY/AGENT INFORMATION:

NAME: Steife, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0470001
 TELECOMMUNICATION INFORMATION:
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 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
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 US-09-345-790-1

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US-09-195-368-1 (1-177) x US-09-345-790-1 (1-1849)

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 QY 21 ArgSerSerTyrLysLeuTyrPhePheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 89 AGATCATCCCTGGAAGCTGTGGCTCTTTGCTCAATGATGATGTTGCTATTTCTTCTCTCC 148
 QY 41 PheSerThrPheLeuPheIlePheLeuGlnIleuGlnThrAlaIleGluProCysMetAla 60
 DB 149 TTGAGTGGCTAATCTTATTTTCTCAATTAAGAAGCTTAAGAGCCCTGTATGGCT 208
 QY 61 LysPheGlyProLeuProSerLysTyrGlnMetAlaSerSerGluProProCysValAsn 80
 DB 209 AAGTTTGACCATTTACCTCAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 268
 QY 81 LysValSerAspTyrPheLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
 DB 269 AAGGTGTCTGACTGGAAGCTGAGATGACTTCAGAAATGCTTATATTTATTTATGCGCAA 328
 QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
 DB 329 GTGGCTCCCAATGCAAACTCAATGATGAGTCTCTTTGAGTGGCGCTGATTAATAAC 388
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
 DB 389 AAAGCATGATCAAACTCACTAACAACAATCTAAATCCAAATGATGAGGAGCACTTAT 448
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGluValLeuLys 160
 DB 449 GAATTCAGATGTGGGACCACTGATGATTTCACTGACATCGACATCGAGTTCTAAAA 508
 QY 161 AsnAsnThrTyrTyrGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 509 AATAATACCTAGTGGGTATCATTTTACTAGCAAAATCCCAATTCATCTCC 559

RESULT 4

US-09-620-312D-30
 ; Sequence 30, Application US/09620312D
 ; Patent No. 6569662

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod
 APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhilwei
 APPLICANT: John Tilihnphast
 APPLICANT: Dmanac, Radoje T.
 TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 FILE REFERENCE: Polypeptides

CURRENT APPLICATION NUMBER: US/09/620,312D

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105

QY 73 SerSerGIuProCYsValAlaSerValSerAspTrp-----LysLeu 87
 Db 272 TGAAGAAGCACCCTGT-----TGAATATTATGTAAAGCGAAGT 313
 QY 88 GluIleuGlnAenGlyLeuTyrGlyGlnValAlaProAen-AlaAenTyr 107
 Db 314 CAGGTGTCAAGAACCACTGGTATTATTA-----ATAACACCCCATTCACATCT 364
 QY 107 rAspAspVal-----AlaProheGluValArgLeuTyrLysAenLysAspMetile-- 124
 Db 365 TAATTCGTGAAAAAGCTCTTTCAGTGAAGTGTTCAGTGAAGCAATCAGTGTCTGA 424
 QY 125 -----GlnThrLeuThrAenLysSerLysIleGlnAenValGlyGlyThrTyr 140
 Db 425 ACAAGTCATATCTATATACATTAGACATAGCACAAAGATTTCAG-----GGTGTATATA 478
 QY 140 rGluLeuHis 143
 Db 479 TGAACATCAC 488

RESULT 6 US-09-107-532A-305

; Sequence 305, Application US/09107532A
 ; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lytton A Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESSES:
 ADDRESS: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA

ZIP: 02354
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
 NAME: Ariniello, Pamela Deneka
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 305:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3666 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (8) LOCATION 1...3666
 SEQUENCE DESCRIPTION: SEQ ID NO: 305:

US-09-107-532A-305

Alignment Scores:
 Pred. No.: 1.53 Length: 3666
 Score: 84.50 Matches: 19
 Percent Similarity: 57.58% Conservative: 19
 Best Local Similarity: 28.79% Mismatches: 23
 Query Match: 8.89% Indels: 5
 DB: 4 Gaps: 1

US-09-195-368-1 (1-177) x US-09-107-532A-305 (1-3666)

QY 102 AlaProAenAlaAenTyrAspAspValAlaProheGluValArgLeuTyrLysAenLys 121
 Db 1543 GCTCCTAATGGTCTACCAACTAGATTCAAGCGAATTTTCAATTACAGTTAAAGAAATCA 1602

QY 122 AspMetileGlnThrLeuThrAenLysSer-----LysIleGlnAenVal 136
 Db 1603 AATGTACTACCAACAAGAACCAATAGAAATCCACAGGTTCTGTGAATTTGAAAGATA 1662

QY 137 GlyGlyThrTyrGluLeuHisValGlyAspThrIleAspLeuIlePheAenSerGluHis 156
 Db 1663 GGCAGATTAGATGATAGATTGAGACTACCGAATGATGATTCACGATTATATATCCGATTAAC 1722

QY 157 GlnValLeuLysAspAen 162
 Db 1723 AAAGTTGTTAAAGATAAC 1740

RESULT 7 US-09-621-976-13182

; Sequence 13182, Application US/09621976
 ; Patent No. 6639063

GENERAL INFORMATION:
 APPLICANT: Dumas Malne Edwards, J.B.
 APPLICANT: Jobert, S.
 APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: GENSET.054PR2
 CURRENT APPLICATION NUMBER: US/09/621,976
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 19335
 SOFTWARE: Patent.pm
 SEQ ID NO 13182
 LENGTH: 457
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-621-976-13182

Alignment Scores:
 Pred. No.: 0.095 Length: 457
 Score: 82.50 Matches: 41
 Percent Similarity: 37.57% Conservative: 24
 Best Local Similarity: 23.70% Mismatches: 45
 Query Match: 8.68% Indels: 63
 DB: 4 Gaps: 9

US-09-195-368-1 (1-177) x US-09-621-976-13182 (1-457)

QY 6 LeuGlnAsnMetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTrpLys 25
 Db 23 CTCGCCACCGCCGCGGCTGCCCATCTGCTGCGCTGTGGCCAG-----AGCTGGAAA 76

QY 26 LeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeuIle 45
 Db 77 -----GCATGCTGTGG 88

QY 46 PheIlePheLeuGlnLeuGlnThrAlaLysGluProCYs-----AGCTGGCTGTGG 58
 Db 89 TATGATCTTTGGC-----AGCTGGCTGTGG 130

QY 59 -----MetAlaLysPheGlyProLeuProSerLys-----AGCTGGCTGTGG 68
 Db 131 AACGGAACCTCTCTCGGTGTGAGATTGCAAGTTAACTTAAGAAAAACGCAATTCGCAA 190

US-09-107-532A-305

```
QY 69 -----TpgInMetalaserSergIupProCyValaInuYValaSerAspTrp 85
Db 191 ATATTTGCGAAATCTCGGTGATTAAGGCCCATGTACT----- 235
QY 86 LysleuDuIleuGlnAsnGlyLeuTyrLeuIleTyr-Gly---GlnValAlaProAs 104
Db 236 -----TTGCGAGGGGTCTCTGACTGTAGTCTGAGTGTAGATTTTAAAAA 283
QY 104 nalaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsnLysAspMet11 124
Db 284 TCCATCTTATCAAAAATA---CCGTTTAAGTGGAATAATTGCAATGCAAGTCGACGATT 340
QY 124 eGlnThLeuThr-----Aen-LysSerLysIleGlnAsnValGlyG 138
Db 341 GATGAGATTCATTAATATATTTAGATAGATAATAGAGAAAACTACAGTCAGTCATTA 400
QY 138 LyrThyTyrGluLeuHisValGlyAspThrIleAsp 149
Db 401 TTAAGTATTTTTCATATTTTGGGGGATTAAGT 435

RESULT 8
US-09-851-985-3/c
Sequence 3, Application US/09851985
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUMAN RECEPTOR PROTEINS, AND
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN RECEPTOR PROTEINS, AND
FILE REFERENCE: C1001238
CURRENT APPLICATION NUMBER: US/09/851,985
CURRENT FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 21968
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(21968)
OTHER INFORMATION: n = A,T,C or G
US-09-851-985-3

Alignment Scores:
Pred. No.: 99.1 Length: 21968
Score: 80.50 Matches: 29
Percent Similarity: 45.45% Conservative: 11
Best Local Similarity: 32.95% Mismatches: 27
Query Match: 8.46% Indels: 21
DB: 4 Gaps: 5

US-09-195-368-1 (1-177) x US-09-851-985-3 (1-21968)
QY 4 SerHisleuGluAsnMetProleuSerHisSerArgThrGlnGlyAlaGlnArgSerSer 23
Db 17227 TCTTCAACAGAGAACTGAAACGGACAGGGTTGAGGAGAGGGGCCCAAGAGAGAA 17168
QY 24 TrpLysleu-----TrpLeuPheCysSerIleVal-----MetLeu 35
Db 17167 TGGGACATGATTCAGTCTTTCGATGCTCAGAGAGCTCCATGCTCATGCTAGGCTCAAG 17108
QY 36 LeuPheLeuCys-----SerPheSerTrpLeuIlePheIlePheLeuGln 50
Db 17107 GTCTTCTCTGCAAGGCTGATCCCTCTCCCTTTTAACTTAAAGTCATCTCTCTCG 17048
QY 51 LeuGlnThrAlaLysGluProCysMetalAlaLysPheGlyProleuProSerLysTrpGln 70
Db 17047 CACGACGCTACGCCAGCT-----GTGCACTGGGCAACCTTTCATCATTTATCA 16934
QY 71 MetalaserSergIupProCy 78
Db 16993 -----CCATGC 16988
```

```
RESULT 9
US-09-230-380-10
Sequence 10, Application US/09230380A
GENERAL INFORMATION:
APPLICANT: Keshi, Hiroyuki
APPLICANT: Eda, Soji
APPLICANT: Uehara, Hirotatsu
APPLICANT: Nishida, Keigo
APPLICANT: Matsuhisa, Akio
TITLE OF INVENTION: Probes For Detecting and Identifying Helicobacter
FILE REFERENCE: 19036/35268
CURRENT APPLICATION NUMBER: US/09/230,380A
CURRENT FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 1219
TYPE: DNA
ORGANISM: Helicobacter pylori
US-09-230-380-10

Alignment Scores:
Pred. No.: 1.03 Length: 1219
Score: 80.00 Matches: 37
Percent Similarity: 37.57% Conservative: 28
Best Local Similarity: 21.39% Mismatches: 58
Query Match: 8.41% Indels: 50
DB: 3 Gaps: 8

US-09-195-368-1 (1-177) x US-09-230-380-10 (1-1219)
QY 13 HisSerArgThrGlnGlyAlaGlnArgSerSerTrpLysleuTrpLeuPheCysSerIle 32
Db 361 CATTTAAAGGCAAGCATGATGATTAATCTCAAAATTTGGCTGTCCTTACCAT 420
QY 33 ValMetLeuLeuPheLeuCysSerPheSerTrpGlnMetAlaSerSergIupProCyValAsn 50
Db 421 TGCTTTTGTGTTGTGTATTTATTTTAAATTTTGTGATGTTTATGTTTAAAGTTTG 480
QY 51 -----LeuGluThrAlaLysGluProCysMetalA----- 60
Db 481 CAATGCACATCTTTGCTCTGTGCGACAGAAACGSAACCAACCATCACACACCAAG 540
QY 61 LysPheGlyProleuProSerLysTrpGlnMetalaserSergIupProCyValAsn 80
Db 541 AAATTTGGTAAAGAAATTCGAAACACAG-----ATTCA 573
QY 81 LysValaserAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
Db 574 AAGATC-----CATTAATTTTCTTTTCTTTTGGCGAT 606
QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
Db 607 ACTTGCGGTATGGA-----ATGAATATCAATTA---AAGAT 642
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
Db 643 TTTTCATATGATCATGCGCTTCTCTCTTCCGCGTGCATCTGTGGGGAATTACAG 702
QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSergIu----- 155
Db 703 CGTGTGAAAAGAAATGAAAAAGTTGAA-----AATGACGAGCGCTCTGTATAG 753
QY 156 -----HisGlnValLeuLysAsnThrTyr 164
Db 754 GTGGCTAAATCAACGACGATTTGAAAACACACAGAT 792

RESULT 10
US-09-078-294-13/c
Sequence 13, Application US/09078294
```


NUMBER OF SEQUENCES: 14
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/474,642
 FILING DATE: 29-APR-1985
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 824,704
 FILING DATE: 04-FEB-1987
 SEQ ID NO.1:
 LENGTH: 1062
 5395759-1

Alignment Scores:
 Pred. No.: 2.08 Length: 1062
 Score: 77.00 Matches: 42
 Percent Similarity: 38.59% Conservative: 28
 Best Local Similarity: 22.83% Mismatches: 59
 Query Match: 8.10% Indels: 54
 DB: Gaps: 9

US-09-195-368-1 (1-177) x 5395759-1 (1-1062)

QY 26 LeuTTPleuPheCysSerIleValMetLeuPheLeuCys-----Ser 40
 Db CTGACATTGATTCATCATATTAATTAATAAACTAATACTAATACG 135
 QY 41 PheSerTTPleuIlePheIlePheLeuGlnLeuGluThraIalysGluProCysMetAla 60
 Db ATGACATCATATTTTACGTTTACTACTCATGTTTAATATACCCATTGTAGG 135
 QY 61 Lys-----PheGlyProLeuProSerLysTTPGlnMet 71
 Db ACACAAATTAATGCGATGATTTTACCAATAACGGGATCATCAGCGCTGATATACGAT 255
 QY 72 AlasSerSerGluProPro-----CysVal----- 79
 Db TCTACTATGAGAGACCACTTTTAACTTCAGCGCTGCTTTTATATCTATCCAGCAAGACT 315
 QY 80 ---AenLysValSerAspTTPlysLeuGlnIleLeuGlnAengLysLeuTyrLeuIleTyr 98
 Db AAAATAGATTCATGATGATGAATGGGAAATACCTTATCAATATTTTACTGAAA 375
 QY 99 GlnValAlaIleProAenAla-----AsnTyrAsnAspValAlaIleProPheGlnVal 115
 Db GAGAGGCCAATGATGATGATTTTAAAGACTCAATGATATTAATCAATTTTCTGTG 435
 QY 116 -----ArgLeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIle 133
 Db AATCACAACATATTTGATTAATATAGTAGTA-----TTG 471
 QY 134 GlnAsnValGlyGlyThrTyrGlnLeuHisValGlyAspThrIleAspLeuIlePheAsn 153
 Db ATGAGATATGACAATACATCTGAAATGATGATGATGATGATGATGATGATGATGAT 531
 QY 154 SerGluHisGlnValLeuLysAsnAsnThrTyrTTPGlyIleIleLeuLeuAlaAsnPro 173
 Db 532 GAA-----TTG-----CTGTGCAATCT 549
 QY 174 GlnPheIleSer 177
 Db 550 ATGATATATCG 561

RESULT 15

US-09-976-594-668/C
 Sequence 668, Application US/09976594
 Patent No. 6673549
 GENERAL INFORMATION:
 APPLICANT: Furness, Michael
 APPLICANT: Buchinder, Jenny
 TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 FILE REFERENCE: PA-0041 US
 CURRENT APPLICATION NUMBER: US/09/976,594
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/240,409

PRIOR FILING DATE: 2000-10-12
 NUMBER OF SEQ ID NOS: 1143
 SOFTWARE: PERL Program
 SEQ ID NO 668
 LENGTH: 4446
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc.feature
 OTHER INFORMATION: Incyte ID No. 6673549 001322.4
 US-09-976-594-668

Alignment Scores:
 Pred. No.: 21.6 Length: 4446
 Score: 77.00 Matches: 37
 Percent Similarity: 35.56% Conservative: 11
 Best Local Similarity: 27.41% Mismatches: 35
 Query Match: 8.10% Indels: 52
 DB: Gaps: 8

US-09-195-368-1 (1-177) x US-09-976-594-668 (1-4446)

QY 3 LeuSerHis---LeuGlnAsnMetProLeuSerHisSerArgThrGlnIalaglArg 21
 Db TTAAGCACCTCTTCTCCATTCCTCCATCAGGCTCTTACACAACAACCACTCTTGA 363
 QY 22 SerSerTTPlysLeuTTPleuPheCysSerIleValMetLeuLeuPheLeuCysSer--- 40
 Db TCTTCT-----TGGCTGTTT---TCACAGATTCTTGATGTTTCTAGTTCTATC 315
 QY 40 ----- 40
 Db CATAGCTTCATAGATATGATTCATCAAGAATCTGGGAAATGATGATCAATGGA 255
 QY 41 -----PheSerTTPleuIle-----PheIlePheLeu 49
 Db GGCCTTCATACACTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG 195
 QY 50 GlnLeuGluThraIalLysGlnProCysMetAlalysPheGlyPro-----Leu 65
 Db CGACTGAGAGGTGGCTTCCCTCCCTGCTTGGATGCGCTGCCAGGCGCTGATCTG 135
 QY 66 ProSerLysTTPGlnMetAlaSerSerGluProProCysValAsnLysValSerAspTTP 85
 Db CCGCTGGGGGTGTAGGCTGTTAGTCACTCC-----TTG 99
 QY 86 LysLeuGlu-----IleLeuGlnAengLysLeuTyrLeuIle 97
 Db GAACTGAGAGCCAGCTCATGTGTGAGAGAGGACATATCTTCTG 54

Search completed: April 7, 2004, 21:12:08
 Job time: 87.0684 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:55:16 ; Search time 2642.89 Seconds

(without alignments)
2502.773 Million cell updates/sec

Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLNMPLSHSRTOGAQ.....VLKNTYWGILLANPOFIS 177

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 2167151695 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=genembl -O=FASTA -SUFFIX=ysge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCU=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09195368 @CGN 1.1 5417 @runat.07042004.061638.2594 -NCPU=6 -ICPU=3
-NO MAP -LARGESUBSTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl: *
1: gb_da: *
2: gb_hcg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_ov: *
22: em_ov: *
23: em_pac: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	534	9 AF125303	AF125303 Homo sapi
2	951	100.0	1849	6 AR092586	AR092586 Sequence
3	951	100.0	1849	6 BD268764	BD268764 Human end
4	951	100.0	1849	6 AR214043	AR214043 Sequence
5	951	100.0	1849	6 AR282586	AR282586 Sequence
6	951	100.0	1964	6 AX074393	AX074393 Sequence
7	951	100.0	1964	6 AX077015	AX077015 Sequence
8	951	100.0	1964	6 AX080755	AX080755 Sequence
9	951	100.0	1964	6 AX150805	AX150805 Sequence
10	951	100.0	1964	6 AX391258	AX391258 Sequence
11	951	100.0	1964	6 BD085933	BD085933 Tumor nec
12	951	100.0	1964	6 BD124038	BD124038 Novel tum
13	951	100.0	1964	6 BD124046	BD124046 Novel tum
14	951	100.0	1964	6 AY358868	AY358868 Homo sapi
15	906	95.3	510	9 AF117713	AF117713 Homo sapi
16	628	66.0	1633	9 HS15D23	HS15D23
17	419.5	44.1	568	10 AY234223	AY234223 Mus muscu
18	419.5	44.1	1261	10 MM0577580	MM0577580 Mus muscu
19	419.5	44.1	2066	10 MM0577579	MM0577579 Mus muscu
20	414.5	43.6	522	10 AY267900	AY267900 Mus muscu
21	413.5	43.5	528	10 AY320040	AY320040 Mus muscu
22	412.5	43.4	522	10 AY359852	AY359852 Mus muscu
23	333.5	33.1	2281	2 AC109057	AC109057 Rattus no
24	317.5	33.4	1161	2 AC117819	AC117819 Mus muscu
25	108.5	11.4	892	5 GGN24435	GN24435 Gallus ga
26	106.5	11.2	2485	2 AC112050	AC112050 Rattus no
27	106.5	11.2	2831	2 AC131215	AC131215 Rattus no
28	103.5	10.9	1789	10 AL668897	AL668897 Mouse DNA
29	99.5	10.5	1827	10 AL772354	AL772354 Mouse DNA
30	98.5	10.4	7861	9 AC000398	AC000398 Genomic s
31	98	10.3	1402	9 HSDJ40724	HSJ40724 Human DNA
32	98	10.3	2530	2 AC095864	AC095864 Rattus no
33	97.5	10.3	2548	2 AC103318	AC103318 Rattus no
34	97.5	10.3	1650	2 AC037468	AC037468 Homo sapi
35	97.5	10.3	1690	9 AC098677	AC098677 Homo sapi
36	97.5	10.3	1714	9 AC092701	AC092701 Homo sapi
37	97.5	10.3	1730	2 AC069320	AC069320 Homo sapi
38	97.5	10.3	1792	2 AC090070	AC090070 Homo sapi
39	97	10.2	1530	2 AC022044	AC022044 Homo sapi
40	97	10.2	1532	2 AC060758	AC060758 Homo sapi
41	95.5	10.0	1892	9 AC020595	AC020595 Homo sapi
42	95.5	10.0	6779	2 AC016116	AC016116 Homo sapi
43	95.5	10.0	1249	9 AJ358794	AJ358794 Human DNA
44	95.5	10.0	3000	9 AB100084	AB100084 Pan trogl
45	95	10.0	1660	2 AC023645	AC023645 Homo sapi

RESULT 1

ALIGNMENTS

AF125303 534 bp mRNA linear PRI 02-APR-1999
 LOCUS AF125303 Homo sapiens glucocorticoid-induced TNFR-related protein ligand
 DEFINITION (TNFSF18) mRNA, complete cds.
 ACCESSION AF125303
 VERSION AF125303.1 GI:4558500
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 534)
 AUTHORS Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,
 Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
 Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J., and Ashkenazi,A.
 Identification of a new member of the tumor necrosis factor family
 and its receptor, a human ortholog of mouse GITR
 Curr. Biol. (1999) In press
 2 (bases 1 to 534)
 Gurney,A.L., Masters,S.A., Huang,A., Pitti,R.M., Mark,M.,
 Baldwin,D.T., Gray,A.M., Dowd,P., Brush,J., Heldens,S., Schow,P.,
 Goddard,A.D., Wood,W.I., Baker,K.P., Godowski,P.J., and Ashkenazi,A.
 Direct Submission
 Submitted (01-FEB-1999) Molecular Oncology, Genentech, 1 DNA Way,
 South San Francisco, CA 94080, USA
 FEATURES
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 1..534
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 /product="glucocorticoid-induced TNFR-related protein
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 /db_xref="GI:4558501"
 /translation="MCLSHLEMPISHSRTGAGRSSWKLWLFCSIYVLLFCSFSL
 IPIQLTAKPEPKAVKRPSPKQNASSEPCVKNVSDWKEIILNGYLLIGQVA
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 NNTYGIILANPDIS"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3,636-97 Length: 534
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
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 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgTrpGlnGlyAlaGln 20
 DB 1 ATGTGTTGAGCACTTGCAAAATATGCTTTAAGCCATTCAAGACTCAAGAGCTCAG 60
 QY 21 ArgSerSerTrpLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 61 AGATATCTCGAAGACTGGCTCTTTGCTCAATAGTATGTTGCTATTCTTGGCTCC 120
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluTrpAlaValGluProCysMetAla 60
 DB 121 TTCAGTGGCTAACTTTATTTTCTCCATTAGAGAGTGTCAAGAGCCCTGTATGCT 180
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80

DB 181 AAGTTGACCACTTACCTCAAAATGCAATGGCAATGGCATCTTCTGACCTCTTGGCAAT 240
 QY 81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrlleuIleTyrlGln 100
 DB 241 AAGGTGTCTACCTGGAAGCTGGAGATCTTCAGAAATGGCTTATATTATTTATGGCCAA 300
 QY 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGluValAlaArgLeuTyrlAsn 120
 DB 301 GTGGCTCCCAATCAACCAATCAATGATGTAGTCCCTTTGAGGTGGCTGTATTAAGC 360
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyIleTyrl 140
 DB 361 AAAGACATGATACCAACTTCAACCAACCAATCTAAATCCAAATGTAGAGGACTTAT 420
 QY 141 GluLeuHisValGlyAspTrpIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 DB 421 GAATGCACTTGGGAGACCACTAGACTTGATTTCACTTGAGCATCAGGTTCTAAAA 480
 QY 161 AsnAsnThrTyrlTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 481 AATAATACATACATGGGGTATCATTTTACTAGCAAAATCCCAATTCATCTCC 531
 RESULT 2
 LOCUS AR092586 1849 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 1 from patent US 5998171.
 ACCESSION AR092586
 VERSION AR092586.1 GI:10019339
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1849)
 AUTHORS Yu,G.-L., Ni,J., and Rosen,C.A.
 TITLE Polynucleotides encoding human endokine alpha
 JOURNAL Patent: US 5998171-A 1 07-DEC-1999;
 FEATURES
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 /mol_type="unassigned DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,786-96 Length: 1849
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-195-368-1 (1-177) x AR092586 (1-1849)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgTrpGlnGlyAlaGln 20
 DB 29 ATGTGTTGAGCACTTGCAAAATATGCTTTAAGCCATTCAAGACTCAAGAGCTCAG 88
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 89 AGATATCTCGAAGACTGGCTCTTTGCTCAATAGTATGTTGCTATTCTTGGCTCC 148
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluTrpAlaValGluProCysMetAla 60
 DB 149 TTCAGTGGCTAACTTTATTTTCTCCATTAGAGAGTGTCAAGAGCCCTGTATGCT 208
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 DB 209 AAGTTGACCACTTACCTCAAAATGCAATGGCAATGGCATCTTGTGAACCTCTTGGCTGAT 268
 QY 81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrlleuIleTyrlGln 100
 DB 269 AAGGTGTCTACCTGGAAGCTGGAGATCTTCAGAAATGGCTTATATTATTTATGGCCAA 328

QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
Db 329 GTGGCTCCCAATGCAAACTGCAATGATGAGTGCCTTTTGAAGGCGCGTATATAAAC 388
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
Db 389 AAAGACATGATACAACTCTTAACAAACAAATCTTAATCCAAATGTAAGAGGACTTAT 448
QY 141 GlnLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
Db 449 GAATGGATGATGGGACACCATGACTTATATTCAGACTGACATCGGTTCTPAAA 508
QY 161 AsnAsnThrTyrTyrGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db 509 AATAATACCTACTGGGATCATTTTACTACGAAATCCCAATTCATCTCC 559

RESULT 3
LOCUS BD268764 1849 bp DNA linear PAT 17-JUL-2003
DEFINITION Human endokine alpha and methods of use.
ACCESSION BD268764.1 GI:33078532
VERSION JP 2002537769-A/1.
KEYWORDS JP 2002537769-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1849)
AUTHORS Yu, G.-L., Ni, J. and Rosen, C.A.
TITLE Human endokine alpha and methods of use
JOURNAL Patent: JP 2002537769-A 1 12-NOV-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Artificial Sequence
PN JP 2002537769-A/1
PD 12-NOV-2002
PR 25-FEB-2000 JP 2000601183
PR 26-FEB-1999 US 60/123099 28-MAY-1999 US 60/136788 PI
GEO L1ANG YT/JTAN NI, CRAIG A ROSEN
PC C12N15/09, A61K38/22, A61K39/395, A61K39/395, A61K45/00, A61P1/00,
PC A61P1/16,
PC A61P3/00, A61P3/08, A61P5/14, A61P7/06, A61P9/10, A61P11/06 PC
A61P13/12, A61P17/02,
PC A61P17/06, A61P19/00, A61P19/02, A61P21/04, A61P25/00, A61P25/00,
PC A61P25/16,
PC A61P25/28, A61P27/02, A61P29/00, A61P31/04, A61P33/00, A61P35/00,
PC A61P35/02,
PC A61P37/02, A61P37/04, A61P37/06, A61P37/08, A61P43/00, C07K14/52,
PC C07K16/24,
PC C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12N15/00, C12N5/
PC 00 A61K37/24
CC endokine alpha protein
FH key
FT CDS Location/Qualifiers
1..1849
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Alignment Scores:
Pred. No.: 1.78e-36 Length: 1849
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-195-368-1 (1-177) x BD268764 (1-1849)

QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
Db 29 ATGTGTTGAGCCACTTGGAATAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 88

QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db 89 AGATATCTCGAAGCTTGAGCTCTTTGCTCCATAGTATGTTGCTATTTCTTCTCC 148
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
Db 149 TTCAGTTGGCTAATCTTATTTTCTCCATTAGAGACTGTAAGAGCCCTGATAGCT 208
QY 61 LysPheGlyProLeuProSerLysTrpGlnMetLysSerArgLysProPheCysValAsn 80
Db 209 AAGTTGACCATTAACCTCAAAATGGCAATGGATTTCTGAACCTCTTGCGGTGAT 268
QY 81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrLeuIleTyrGln 100
Db 269 AAGGTGCTGAGCTGGAAGCTGGAAGTACTGAGATGCTTATATTATTTATAGGCCAA 328
QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
Db 329 GTGGCTCCCAATGCAAACTGCAATGATGAGTGCCTTTTGAAGGCGCGTATATAAAC 388
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
Db 389 AAAGACATGATACAACTCTTAACAAACAAATCTTAATCCAAATGTAAGAGGACTTAT 448
QY 141 GlnLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
Db 449 GAATGGATGATGGGACACCATGACTGATATTCAGACTGACATCGGTTCTPAAA 508
QY 161 AsnAsnThrTyrTyrGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db 509 AATAATACCTACTGGGATCATTTTACTACGAAATCCCAATTCATCTCC 559

RESULT 4
LOCUS AR214043 1849 bp mRNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6406867.
ACCESSION AR214043
VERSION AR214043.1 GI:23311480
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1849)
AUTHORS Yu, G.-L., Ni, J. and Rosen, C.A.
TITLE Antibody to human endokine alpha and methods of use
JOURNAL Patent: US 6406867-A 1 18-JUN-2002;
FEATURES
source Location/Qualifiers
1..1849
/organism="unknown"
/mol_type="mRNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.78e-96 Length: 1849
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6

US-09-195-368-1 (1-177) x AR214043 (1-1849)

QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
Db 29 ATGTGTTGAGCCACTTGGAATAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 88
QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db 89 AGATATCTCGAAGCTTGAGCTCTTTGCTCCATAGTATGTTGCTATTTCTTCTCC 148
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
Db 149 TTCAGTTGGCTAATCTTATTTTCTCCATTAGAGACTGTAAGAGCCCTGATAGCT 208

QY 61 LysPheGlyProLeuProSerIysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 209 AAGTTTGACCATTAACCTCAAAATGCAATGCGATCTTTCGAACCTCTGGCGAAT 268
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
 Db 269 AAGGTGTCTGACTGAAAGCTGGAGATACCTCAAGATGGCTTATTAATTAATGACCA 328
 QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValArgLeuTyrLysAsn 120
 Db 329 GTGGCTCCCATGCAACATCAATGATGATGATGCTCTTTGAGGTGGCTGTATTAAC 388
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
 Db 389 AAAGACATGATACCAACTCTCAACAACTCAAAATCCAAATGTAGAGGACTTAT 448
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 449 GAATTGATGTTGGGACACCATAGACTTGAATTTCACTTCGAGCATCAGGTTCTAA 508
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 509 AATTAATACCTACGCGGTATCAATTTACTAGCAAAATCCCAATTCATCTCC 559
 RESULT 5
 LOCUS AR282586 1849 bp mRNA linear PAT 10-APR-2003
 DEFINITION Sequence 1 from patent US 6521742.
 ACCESSION AR282586
 VERSION AR282586.1 GI:29719155
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1849)
 AUTHORS Yu, G.-L., Ni, J. and Rosen, C. A.
 TITLE Human endokine alpha
 JOURNAL Patent: US 6521742-A 18-FEB-2003;
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 source 1. 1849
 Location/Qualifiers
 /organism="unknown"
 /mol_type="mRNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.78e-96 Length: 1849
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-195-368-1 (1-177) x AR282586 (1-1849)

QY 1 MetCysLeuSerHisLeuGlnAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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 Db 89 AGATCATCTCGAAGCTGTGGCTCTTTGCTCAATGATATGTGTATTTCTTTGCTCC 148
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGluProCysMetAla 60
 Db 149 TTCAAGTGGCTAATCTTATTTTTCCTCAATTAGACATGCTPAAGAGGCTGTATGGCT 208
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 209 AAGTTTGACCATTAACCTCAAAATGCAATGCGATCTTTCGAACCTCTGGCGAAT 268
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Db 269 AAGGTGTCTGACTGAAAGCTGGAGATACCTCAAGATGGCTTATTAATTAATGACCA 328
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 Db 329 GTGGCTCCCATGCAACATCAATGATGATGATGCTCTTTGAGGTGGCTGTATTAAC 388
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
 Db 389 AAAGACATGATACCAACTCTCAACAACTCAAAATCCAAATGTAGAGGACTTAT 448
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 449 GAATTGATGTTGGGACACCATAGACTTGAATTTCACTTCGAGCATCAGGTTCTAA 508
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 509 AATTAATACCTACGCGGTATCAATTTACTAGCAAAATCCCAATTCATCTCC 559
 RESULT 6
 LOCUS AX074393 1964 bp DNA linear PAT 06-FEB-2001
 DEFINITION Sequence 13 from Patent WO0103720.
 ACCESSION AX074393
 VERSION AX074393.1 GI:12710533
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Williams, P.M. and Gerzitsen, M.E.
 TITLE Promotion or inhibition of angiogenesis and cardiovascularization
 JOURNAL by tumor necrosis factor ligand/receptor homologs
 Patent: WO 0103720-A 13 JAN-2001;
 FEATURES
 Location/Qualifiers
 source 1. 1964
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.93e-96 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-195-368-1 (1-177) x AX074393 (1-1964)

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 Db 21 ATGTGTTTGAAGCCACTTGAAATATAGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 80
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 Db 81 AGATCATCTCGAAGCTGTGGCTCTTTGCTCAATGATATGTGTATTTCTTTGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGluProCysMetAla 60
 Db 141 TTCAAGTGGCTAATCTTATTTTTCCTCAATTAGACATGCTPAAGAGGCTGTATGGCT 200
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 201 AAGTTTGACCATTAACCTCAAAATGCAATGCGATCTTTCGAACCTCTGGCGAAT 260
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
 Db 261 AAGGTGTCTGACTGAAAGCTGGAGATACCTCAAGATGGCTTATTAATTAATGACCA 320
 QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValArgLeuTyrLysAsn 120

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Db      321 GTGGCTCCCAATGCACAACTACAAATGATGATGACTCTCTTTGAGTGCGGCGCTGATATAAAC 380
Qy      121 LysAspMetIleGlnThrLeuThraSnlYserLysIleGlnAsnValGlyGlyThrTyr 140
Db      381 AAAGACATGATCAAACTCTAACAAACAAATCTAAATCCAAATGTAGAGGGGACTTAT 440
Qy      141 GlnLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
Db      441 GAATTCATGTTGGGACACCATGACTGATGATTCACCTTGAGCATCAGGTTCTTAAAA 500
Qy      161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db      501 AATAATACATCTGGGGTATCATTTTACTACCAATCCCAATTCATCTCC 551

RESULT 7
AX077015      1964 bp      DNA      linear      PAT 22-FEB-2001
LOCUS      AX077015
DEFINITION      Sequence 3 from Patent WO0105972.
ACCESSION      AX077015
VERSION      AX077015.1 GI:13121653
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 Ashkenazi, A.U., Baker, K.P., Pong, S., Goddard, A., Godowski, P.J.,
              Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,
              Tunas, D., Watanabe, C.K. and Wood, W.I.
              Compositions and methods for the treatment of immune related
              diseases
              Patent: WO 0105972-A 3 25-JAN-2001;
              Genentech, Inc. (US)
FEATURES
  source      location/Qualifiers
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      1,93e-96      Length:      1964
Score:      951.00      Matches:      177
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0

US-09-195-368-1 (1-177) x AX077015 (1-1964)
Qy      1 MetCysLeuSerHisLeuGlnAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
Db      21 ATGTTGTTAGGACCACTTGAAAAATATGCTTTAAGCCATTCAGAACCTCAGAGGAGCTCAG 80
Qy      21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db      81 AGATCATCTCGAAGCTGAGCTCTTTGCTCAATAGTAGTAGTGTGCTATTCTTGGCTCC 140
Qy      41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnIleThrAlaLysGluProCysMetAla 60
Db      141 TTCAGTTGGCTAATCTTTATTTTCTCCAAATTAGAGACTGCTAAGAGAGCCCTGTATGGCT 200
Qy      61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
Db      201 AAGTTGGACCATTAACCTCAAAATGGCAAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260
Qy      81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
Db      261 AAGGTGCTGACTGGAAGCTGAGATGATCTTCAGAAATGCTTATATTATTTATATGCGCAA 320
Qy      101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120

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Db      321 GTGGCTCCCAATGCACAACTACAAATGATGATGACTCTCTTTGAGTGCGGCGCTGATATAAAC 380
Qy      121 LysAspMetIleGlnThrLeuThraSnlYserLysIleGlnAsnValGlyGlyThrTyr 140
Db      381 AAAGACATGATCAAACTCTAACAAACAAATCTAAATCCAAATGTAGAGGGGACTTAT 440
Qy      141 GlnLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
Db      441 GAATTCATGTTGGGACACCATGACTGATGATTCACCTTGAGCATCAGGTTCTTAAAA 500
Qy      161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db      501 AATAATACATCTGGGGTATCATTTTACTACCAATCCCAATTCATCTCC 551

RESULT 8
AX080755      1964 bp      DNA      linear      PAT 27-FEB-2001
LOCUS      AX080755
DEFINITION      Sequence 1 from Patent WO0109327.
ACCESSION      AX080755
VERSION      AX080755.1 GI:13169735
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 Ashkenazi, A.U., Baker, K.P., Pong, S., Goddard, A., Godowski, P.J., Gurney, A.L.,
              Klievin, I.J., Lafleur, M., Mark, M.R., Marsters, S.A., Pitti, R.M.,
              Watanabe, C.K. and Wood, W.I.
              Method of preventing the injury or death of retinal cells and
              treating ocular diseases
              Patent: WO 0109327-A 1 08-FEB-2001;
              Genentech, Inc. (US)
FEATURES
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              1..1964
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.:      1,93e-96      Length:      1964
Score:      951.00      Matches:      177
Percent Similarity:      100.00%      Conservative:      0
Best Local Similarity:      100.00%      Mismatches:      0
Query Match:      100.00%      Indels:      0
DB:      6      Gaps:      0

US-09-195-368-1 (1-177) x AX080755 (1-1964)
Qy      1 MetCysLeuSerHisLeuGlnAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
Db      21 ATGTTGTTAGGACCACTTGAAAAATATGCTTTAAGCCATTCAGAACCTCAGAGGAGCTCAG 80
Qy      21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db      81 AGATCATCTCGAAGCTGAGCTCTTTGCTCAATAGTAGTAGTGTGCTATTCTTGGCTCC 140
Qy      41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnIleThrAlaLysGluProCysMetAla 60
Db      141 TTCAGTTGGCTAATCTTTATTTTCTCCAAATTAGAGACTGCTAAGAGAGCCCTGTATGGCT 200
Qy      61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
Db      201 AAGTTGGACCATTAACCTCAAAATGGCAAAATGGCATCTTCTGAACCTCCTTGCGTGAAT 260
Qy      81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
Db      261 AAGGTGCTGACTGGAAGCTGAGATGATCTTCAGAAATGCTTATATTATTTATATGCGCAA 320
Qy      101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
Db      321 GTGGCTCCCAATGCACAACTACAAATGATGATGACTCTCTTTGAGTGCGGCGCTGATATAAAC 380

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QY 121 Lysaspmetileglnthrlleuthraenlyserlylelglnasnvalglylythrtyr 140
 Db 381 AAAGACATGATACAACTCTACCAACAAATCTAAATCCAAATATGAGAGGACTTAT 440
 QY 141 Glueuhisvalglyasptthrleaspleuilepheasnsergluhileglnalleuys 160
 Db 441 GAATTGCATGTGGGGACACCATAGACTTATTTCACTCTGAGCATCAGGTTCTTAAA 500
 QY 161 Asnbanthryttrpglylleileleuaualeasnproglinphelieser 177
 Db 501 AATATACATACATCGGGTATCATTTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 9
 AX150805
 LOCUS AX150805 1964 bp DNA linear PAT 22-JUN-2001
 DEFINITION Sequence 1 from Patent WO0140464.
 AX150805
 VERSION AX150805.1 GI:14533039
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Ashkenazi, A.J., Baker, K.P., Ferrara, N., Godowski, P.J., Gurney, A.L.,
 Hillan, K.J., Mark, M.R., Marsters, S.A., Paoni, N.F., Pitti, R.M. and
 Wood, W.I.
 Interleukin-1-receptor associated kinase-3 (Irak3) and its use in
 promotion or inhibition of angiogenesis and cardiovascularization
 Patent: WO 0140464-A 1 07-JUN-2001;
 Genentech, Inc. (US)
 Location/Qualifiers
 1. 1964
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source

ORIGIN

Alignment Scores:
 Pred. No.: 1,93e-96 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-195-368-1 (1-177) x AX150805 (1-1964)

QY 1 MetCysleuSerHisleuGluasnMetProleuSerHisSerArgThrGlnGlyAlaGln 20
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 QY 21 ArgSerSerTrpLysleuTrpLeupheCysSerileValMetleuLeupheleuysSer 40
 Db 81 AGATCATCTCGAAGCTGTGGCTCTTTGCTCAATGATATGTTGCTATTTTGGCTCC 140
 QY 41 PheserTrpleuilepheleleuGlnleuGlnuthAlaIysGluProCysMetAla 60
 Db 141 TTCAAGTGGCTAATCTTATTTTTCCTCAATTAGAACACTGCTAAGAGCCCTGTATGGCT 200
 QY 61 LysPheGlyProleuProSerLysTrpGlnMetAlaSerSerGluProProCysValasn 80
 Db 201 AAGTTTGAGACATTAACCTCAAAATGGCAATGGCATCTTCGACCTCTGGCTGAAT 260
 QY 81 LysValSerAspTrpLysleuGlnulleuGlnasnGlyLeuTryleuileTyrglyGln 100
 Db 261 AAGGTGTCTACGCGAAGCTGAGATACCTTCAGAAATGGCTTATATTATTTATGCGCAA 320
 QY 101 ValAlaProasnAlaasnTyraasnAPValAlaProPheGluValArgleuTyrlvsasn 120
 Db 321 GTGGCTCCCAATGCAACATCAATGATGATAGCTCTTTTGAAGGTGGCTGTATATAAAC 380

QY 121 Lysaspmetileglnthrlleuthraenlyserlylelglnasnvalglylythrtyr 140
 Db 381 AAAGACATGATACAACTCTACCAACAAATCTAAATCCAAATATGAGAGGACTTAT 440
 QY 141 Glueuhisvalglyasptthrleaspleuilepheasnsergluhileglnalleuys 160
 Db 441 GAATTGCATGTGGGGACACCATAGACTTATTTCACTCTGAGCATCAGGTTCTTAAA 500
 QY 161 Asnbanthryttrpglylleileleuaualeasnproglinphelieser 177
 Db 501 AATATACATACATCGGGTATCATTTTACTAGCAAAATCCCAATTCATCTCC 551

RESULT 10
 AX391258
 LOCUS AX391258 1964 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 1 from Patent WO0073445.
 AX391258
 VERSION AX391258.1 GI:19699932
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., Goddard, A.,
 Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marsters, S.A.,
 Pitti, R.M., Wood, W.I., Gerber, H., Gertsen, M.E., Paoni, N.F. and
 Maranabe, C.K.
 Promotion or inhibition of angiogenesis and cardiovascularization
 Patent: WO 0073445-A 1 07-DEC-2000;
 Genentech Inc. (US)
 Location/Qualifiers
 1. 1964
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source

ORIGIN

Alignment Scores:
 Pred. No.: 1,93e-96 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0

US-09-195-368-1 (1-177) x AX391258 (1-1964)

QY 1 MetCysleuSerHisleuGluasnMetProleuSerHisSerArgThrGlnGlyAlaGln 20
 Db 21 ATGTGTTGAGCCACTGGAAATATAGCTTTTAAAGCATTCAGAACTCAAGAGCTCAG 80
 QY 21 ArgSerSerTrpLysleuTrpLeupheCysSerileValMetleuLeupheleuysSer 40
 Db 81 AGATCATCTCGAAGCTGTGGCTCTTTGCTCAATGATATGTTGCTATTTTGGCTCC 140
 QY 41 PheserTrpleuilepheleleuGlnleuGlnuthAlaIysGluProCysMetAla 60
 Db 141 TTCAAGTGGCTAATCTTATTTTTCCTCAATTAGAACACTGCTAAGAGCCCTGTATGGCT 200
 QY 61 LysPheGlyProleuProSerLysTrpGlnMetAlaSerSerGluProProCysValasn 80
 Db 201 AAGTTTGAGACATTAACCTCAAAATGGCAATGGCATCTTCGACCTCTGGCTGAAT 260
 QY 81 LysValSerAspTrpLysleuGlnulleuGlnasnGlyLeuTryleuileTyrglyGln 100
 Db 261 AAGGTGTCTACGCGAAGCTGAGATACCTTCAGAAATGGCTTATATTATTTATGCGCAA 320
 QY 101 ValAlaProasnAlaasnTyraasnAPValAlaProPheGluValArgleuTyrlvsasn 120
 Db 321 GTGGCTCCCAATGCAACATCAATGATGATAGCTCTTTTGAAGGTGGCTGTATATAAAC 380
 QY 121 Lysaspmetileglnthrlleuthraenlyserlylelglnasnvalglylythrtyr 140

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Db      381  AAAGACATGATACAACTTACACAAATCTAAATCCAAATATGAGAGGACTTAT 440
Qy      141  GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
Db      441  GAATTGATTTGGGGGACACCATGACTTATTCACCTGAGCATCAGGTTCTTAAAA 500
Qy      161  AsnAsnThrTyrrTTPGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db      501  AATAATACATACCTGGGGTATCATTTTACTAGCAAAATCCCAATTCACTCC 551

RESULT 11
LOCUS   BD085993                      1964 bp    DNA          linear    PAT 27-AUG-2002
DEFINITION   Tumor necrosis factor homolog DNA19355 polypeptide.
ACCESSION   BD085993.1 GI:22631603
VERSION     BD085993.1
KEYWORDS    JP 2001523459-A/1.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 1964)
AUTHORS    Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Robert, Pitti,
            Baker,K.P., Godowski,P.J. and Mark,M.R.
            Tumor necrosis factor homolog DNA19355 polypeptide
            Patent: JP 2001523459-A 1 27-NOV-2001;
            GENENTECH INC
COMMENT     OS Homo sapiens (human)
            PN JP 2001523459-A/1
            PD 27-NOV-2001
            PF 18-NOV-1998 JP 2000521199
            PR 18-NOV-1997 US 60/065635,12-DEC-1997 US 60/069661 PI
            AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT PI
            PITTI,KEVIN P BAKER.
TITLE      Tumor necrosis factor homolog DNA19355 polypeptide
JOURNAL    GENENTECH INC

FEATURES
source     1. 1964
            Location/Qualifiers
            1..1964
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1,936-96 Length: 1964
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-195-368-1 (1-177) x BD085993 (1-1964)
Qy      1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
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Qy      21 ArgSerSerTyrPlyLeuTyrPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db      81 AGATCATCTCTGGAAGCTGTGGCTCTTTGCTCAATAGTATGTGTCTATTCTTGTCTCC 140
Qy      41 PheSerTyrLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGlnProCysMetAla 60
Db      141 TTCACTGGCTAACTTATTTCTTCTCCATTAAGACTGCTAAGAGCCCTGTATGCT 200

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Qy      61 LysPheGlyProLeuProSerIleTyrGlnMetAlaSerSerGluProProCysValAsn 80
Db      201 AAGTTTGACCATTAACCTCCAAATGCAATGGCATCTTCTGAACTCCCTGGTAAAT 260
Qy      81 LysValSerAspTyrPlyLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
Db      261 AAGGTGCTGACTGGAAGCTGGAGATCTTCAGATGGCTATATTTAATTATGAGCCAA 320
Qy      101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValAlaGlyLeuTyrLysAsn 120
Db      321 GTGGCTCCCAATGCAAACTACATGATGATGAGCTCTTTGAGGCGGCTGTATAAAAAC 380
Qy      121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValGlyIleTyr 140
Db      381 AAAGACATGATACAACTTACACAAATCTAAATCCAAATGTAGAGGAGGACTTAT 440
Qy      141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
Db      441 GAATTGATGTTGGGGGACACCATGACTTGTATTTCAACTGTGACATCAGGTTCTAAAA 500
Qy      161 AsnAsnThrTyrrTTPGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db      501 AATAATACATACCTGGGGTATCATTTTACTAGCAAAATCCCAATTCACTCC 551

RESULT 12
LOCUS   BD124038                      1964 bp    DNA          linear    PAT 18-SEP-2002
DEFINITION   Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same.
ACCESSION   BD124038
VERSION     BD124038.1 GI:23218983
KEYWORDS    JP 2002502607-A/14.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 1964)
AUTHORS    Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Pitti,R.M., Wood,W.I.
            Ashkenazi,A.J., Gurney,A.L., Marsters,S.A., Pitti,R.M., Wood,W.I.
            Novel tumor necrosis factor receptor homolog and nucleic acid
            encoding the same
            Patent: JP 2002502607-A 14 29-JAN-2002;
            GENENTECH INC
COMMENT     OS Homo sapiens (human)
            PN JP 2002502607-A/14
            PD 29-JAN-2002
            PF 09-FEB-1999 JP 2000530610
            PR 09-FEB-1998 US 60/074 087
            PI AVI J ASHKENAZI,AUSTIN L GURNEY,SCOT A MARSTERS,ROBERT M
            PITTI.
TITLE      Novel tumor necrosis factor receptor homolog and nucleic acid
JOURNAL    GENENTECH INC

FEATURES
source     1. 1964
            Location/Qualifiers
            1..1964
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1,936-96 Length: 1964
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0

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Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-195-368-1 (1-177) x BD124038 (1-1964)

QY 1 MetCysLeuSerHisLeuGlnuAnMeCProLeuSerHisSerArgThrGlnGlnValGln 20
 DB 21 ATGTGTTGAGCCACTTGGAATAATGCTTTAAACCTTCAAGAACTCAAGAGGCTCAG 80
 QY 21 ArgSerSerTrpIleuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 81 AGATCATCTGGAAGCTGGGCTCTTTGGCTCAATGTAATGCTGCTATTTCTTGGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnuAlaValGlnProCysMetAla 60
 DB 141 TTCAGTTGGCTATCTTTATTTTCTCCAAATAGAGACTGCTAAGAGCCCTGATAGCT 200
 QY 61 LysPheGlyProLeuProSerIleTrpGlnMetAlaSerSerGlnuProCysValAsn 80
 DB 201 AAGTTTGACCTTACCTCCAAATGGAATGGCAATGGCATCTTCTGAACCTCTTGGCTGAT 260
 QY 81 LysValSerAspTrpIleuGlnuIleLeuGlnuAnGlyLeuTyIleuIleTyIleGln 100
 DB 261 AAGGTCTGACTGGAAGCTGAGATGACTTCAGAAATGGCTTATATTTATTTATGCGCAA 320
 QY 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGlnuValArgLeuTyIleAsn 120
 DB 321 GTGGCTCCCAATGCAAACTACATATGATGCTCTTTGAGGTGGCTGATTAATAAAC 380
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValGlyIleThrTyI 140
 DB 381 AAAGCATGATACCAAACTCTAACAAACAAATCTAAATCCAAATGTAAGAGGACTTAT 440
 QY 141 GluLeuHisValGlyAspThrIleAspIleuIlePheAsnSerGlnuGlnValLeuLys 160
 DB 441 GAATTCAGTGTGGGACACCAATGACTGATGATTTCACTGAGCATCAGGTTCTAAAA 500
 QY 161 AsnAsnThrTyIleGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 501 AATATACACTACTGGGGTATCTTTTACTAGCAATCCCAATCATCTCC 551

RESULT 13
 BD124046 1964 bp DNA linear PAT 18-SEP-2002
 LOCUS BD124046/c
 DEFINITION Novel tumor necrosis factor receptor homolog and nucleic acid
 encoding the same.
 ACCESSION BD124046
 VERSION BD124046.1 GI:23218991
 KEYWORDS UP 2002502607-A/22.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1964)
 Ashkenazi, A.D., Gurney, A.L., Marsters, S.A., Pitti, R.M., Wood, W.I.
 and Goddard, A.V.
 Novel tumor necrosis factor receptor homolog and nucleic acid
 encoding the same
 Patent: JP 2002502607-A 22 29-JAN-2002;
 JOURNAL GENENTECH INC
 OS Homo sapiens (human)
 PN JP 2002502607-A/22
 PD 29-JAN-2002 JP 2000530610
 PF 09-FEB-1999 JP 2000530610
 PR 09-FEB-1998 US 60/074 087
 P1 AVI J ASHKENAZI, AUSTIN L GURNEY, SCOT A MARSTERS, ROBERT M
 PITTI,
 PI WILLIAM I WOOD, AUDLEY GODDARD
 PC C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61P29/00, A61P37/06,
 PC A61P43/00,
 PC C07K14/705, C07K16/28, C07K19/00, C12N1/19, C12N1/21, C12N5/10, PC
 C12P21/02,

PC C12Q1/68//C07K14/47, C12N15/00, A61K37/02, C12N5/00 CC Novel
 tumor necrosis factor receptor homolog and nucleic acid CC
 encoding the
 CC same
 FH Key Location/Qualifiers
 FT source 1.1964
 FT /organism='Homo sapiens'
 /db_xref='taxon:9606'

ORIGIN

Alignment Scores:
 Pred. No.: 1.93e-96 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-195-368-1 (1-177) x BD124046 (1-1964)

QY 1 MetCysLeuSerHisLeuGlnuAnMeCProLeuSerHisSerArgThrGlnGlnValGln 20
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 QY 21 ArgSerSerTrpIleuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
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 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnuAlaValGlnProCysMetAla 60
 DB 1824 TTCAGTTGGCTATCTTTATTTTCTCCAAATAGAGACTGCTAAGAGCCCTGATAGCT 1765
 QY 61 LysPheGlyProLeuProSerIleTrpGlnMetAlaSerSerGlnuProCysValAsn 80
 DB 1764 AAGTTTGACCTTACCTCCAAATGGAATGGCAATGGCATCTTCTGAACCTCTTGGCTGAT 1705
 QY 81 LysValSerAspTrpIleuGlnuIleLeuGlnuAnGlyLeuTyIleuIleTyIleGln 100
 DB 1704 AAGGTCTGACTGGAAGCTGAGATGACTTCAGAAATGGCTTATATTTATTTATGCGCAA 1645
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 DB 1644 GTGGCTCCCAATGCAAACTACATATGATGCTCTTTGAGGTGGCTGATTAATAAAC 1585
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValGlyIleThrTyI 140
 DB 1584 AAAGCATGATACCAAACTCTAACAAACAAATCTAAATCCAAATGTAAGAGGACTTAT 1525
 QY 141 GluLeuHisValGlyAspThrIleAspIleuIlePheAsnSerGlnuGlnValLeuLys 160
 DB 1524 GAATTCAGTGTGGGACACCAATGACTGATGATTTCACTGAGCATCAGGTTCTAAAA 1465
 QY 161 AsnAsnThrTyIleGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 1464 AATATACACTACTGGGGTATCTTTTACTAGCAATCCCAATCATCTCC 1414

RESULT 14
 AY358868 1964 bp mRNA linear PRI 03-OCT-2003
 LOCUS AY358868
 DEFINITION Homo sapiens clone DNA19355 G1TRL (UNC145) mRNA, complete cds.
 ACCESSION AY358868
 VERSION AY358868.1 GI:37182853
 KEYWORDS FLI CDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1964)
 Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,

Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Denel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hase, P. B., Heidens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simons, L., Singh, C., Smith, V., Sincron, J., Vagstad, A., Vanden, R., Watanabe, C., Weiland, K., Xie, M. H., Yasuda, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W. I. and Godowski, P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
PUBMED
12975309
2 (bases 1 to 1964)
AUTHORS
TITLE
DIRECT SUBMISSION
Submitted (01-AGO-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
JOURNAL
Location/Qualifiers

FEATURES
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1. 1964
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/db_xref="taxon:9606"
/clone="DNA1935"
1. 1964
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21. 554
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/note="P19175"
/codon_start=1
/product="GTRFL"
/protein_id="AA089227.1"
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/translation="MCSHLENMPLSHRTQAGQSSWKMLFCSIVMLFCSFSLIFLFIQETAKPCMAKFGPLSPKQWASSPCKVKSQWKEILQNGVLYLGGVA
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NNTWGIILANPQFIS"

ORIGIN
1
MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
21 ATGCTTGAAGCCCTGGAAAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 80
21 ArgSerSerTyrPheLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
81 AGATCATCCTGGAAGCTGTGCTCTTTGCTCAATAGTATGTTGCTATTCTTGCTCC 140
41 PheSerTyrPheLeuPheLeuPheLeuGlnLeuGlnThrAlaGlyGluProCysMetAla 60
141 TTCAGTTGGCAATCTTATTTCTCAATTAAGACTCTAAGAGCCCTTATGGCT 200
61 LysPheGlyProLeuProSerLeuTyrGlnMetAlaSerSerGluProProCysValAsn 80
201 AAGTTTGACCATTAACCTCAAAATGCAATGCACTTCTGAACCTCTTGCTGCTGAAT 260
81 LysValSerAspTyrPheLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
261 AAGGTGCTGCTGAGAGCTGAGATGCTTCAAGATGCTTATATTTAATTTATGGCCA 320
101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValaGlyLeuTyrLeuAsn 120
321 GTGCTCCCATGCAACTCAATGATGATGCTCTTTGAGTGGCGGCTGTATATAAAC 380

US-09-195-368-1 (1-177) x AY358868 (1-1964)

Alignment Scores:
Pred. No.: 1.93e-96 Length: 1964
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValaGlyGlyThrTyr 140
DB 381 AAGGATGATGATCACTTCAACAAACAATCTTAATCCAAATGATGAGAGGACTTAT 440
QY 141 GluLeuHisValaGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
DB 441 GAATGATGATGGGAGACCATGATGATGATTTCAACTGTGAGCATCAGTTCTTAAA 500
QY 161 AsnAsnTyrTyrTyrPheIleIleLeuLeuAlaAsnProGlnPheIleSer 177
DB 501 AATATATACATCTGGGATATCATTTTCTACAAATCCCATTCATCTCTCC 551

RESULT 15
AF117713 510 bp mRNA linear PRI 09-MAR-1999
LOCUS
DEFINITION
AF117713 Homo sapiens A1TR ligand (TL6) mRNA, complete cds.
ACCESSION
AF117713.1 GI:4378801
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 510)
Kwon, B., Yu, K.Y., Ni, J., Yu, G.L., Jang, I.K., Kim, Y.J., Xing, L.,
Liu, D., Wang, S.X. and Kwon, B.S.
Identification of a novel activation-inducible protein of the tumor
necrosis factor receptor superfamily and its ligand
J. Biol. Chem. 274 (10), 6056-6061 (1999)
99156876
10037886
2 (bases 1 to 510)
Kwon, B., Yu, K.Y., Ni, J. and Kwon, B.S.
Direct Submision
Submitted (04-JAN-1999) Micro. & Immunol., Indiana University, 635
Barnhill Dr., Indianapolis, IN 46202, USA
JOURNAL
Location/Qualifiers

FEATURES
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NNTWGIILANPQFIS"

ORIGIN
1
MetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTyrPheLeuTyrPhe 28
QY 9 MetProLeuSerHisSerArgThrGlnGlyAlaGlnArgSerSerTyrPheLeuTyrPhe 28
DB 1 ATGCTTGAAGCCATTCAAGAACTCAAGAGCTCAGATCATCTGGAAGCTGTGCTC 60
QY 29 PheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTyrPheIlePheIlePhe 48
DB 61 TTGCTCAATAGTATGTTGCTATTCTTGCTCTTCAATGCTTATTTT 120

US-09-195-368-1 (1-177) x AF117713 (1-510)

Alignment Scores:
Pred. No.: 3.77e-92 Length: 510
Score: 906.00 Matches: 169
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 95.27% Indels: 0
Gaps: 0

QY 49 LeuGlnLeuGluThrAlaIysGluProCysMetalAlaIysPheGlyProLeuProSerIys 68
 Db 121 CTCGAAATTGAGACTGCTAGAGAGCCCTGTATAGGCTTAAGTTGGACCATTAACCTCAAAA 180
 QY 69 TPGlMetAlaSerSerGluProProCysValAsnIysValSerAspTyrIysLeuGlu 88
 Db 181 TGGCAATGGCATCTTCTGACCTCCTTCCGTGAATAGGTCTGACTGGAAGCTGGAG 240
 QY 89 IleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGlnValAlaProAsnAlaAsnTyrAsn 108
 Db 241 ATAATTGAGAAATGGCTTATATTATATGAGCAAGTGGCTCCCAATGCAAACTACAAAT 300
 QY 109 AspValAlaProPheGluValArgLeuTyrIysAsnIysAspMetIleGlnThrIleThr 128
 Db 301 GATGTAGCTCCCTTTGAGGTGGGCTGTATATAAACAAGACATGATCAAACTCTAACA 360
 QY 129 AsnIysSerIysIleGlnAsnValGlyIleTyrIleLeuHisValGlyAspThrIle 148
 Db 361 AACCAATCTTAAATCCAAATGTAGAGAGGACTTATGAAATTCATGCGGAGACACCAT 420
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 Db 421 GACTGTATATTCACACTGAGCATCAAGTTCTTAAATAAATACTACTGGGGATCATTT 480
 QY 169 LeuLeuAlaAsnProGlnPheIleSer 177
 Db 481 TTACTGGCAATCCCAATTCATCTCC 507

Search completed: April 7, 2004, 18:25:29
 Job time : 2661.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 16:50:59 ; Search time 2423.23 Seconds

(without alignments)
2181.225 Million cell updates/sec

Title: US-09-195-368-1
Perfect score: 951
Sequence: 1 MCLSHLENNPLSHSRGTGAQ.....VLKNTYWGILLANPQFIS 177

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -STAR=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
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6: em_estpl:*
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10: gb_est2:*
11: gb_hic:*
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14: gb_escs:*
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19: em_gss_pln:*
20: em_gss_vit:*
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22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vit:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Query Length	DB ID	Description
1	951	100.0	634 13	BX473859	BX473859 DKFZP686K13165_r1 686 (synonym: hicc3) Homo sapiens CDNA clone
2	608	63.9	669 29	AG182677	AG182677 Pan trogl
3	294	30.9	350 13	BY216375	BY216375 BY216375
4	240	25.2	348 13	BY214208	BY214208 BY214208
5	209.5	22.0	334 13	BY226400	BY226400 BY226400
6	198.5	20.9	328 13	BY326606	BY326606 BY326606
7	194.5	20.5	324 13	BY327839	BY327839 BY327839
8	192.5	20.2	672 29	AG043514	AG043514 Pan trogl
9	117	12.3	114 29	CG977950	CG977950 CH240.168
10	110	11.6	727 13	BU294618	BU294618 603603621
11	110	11.6	731 13	BU373331	BU373331 603589056
12	96	10.1	1514 28	CC250868	CC250868 CH261.178
13	95.5	10.0	842 13	BX709408	BX709408 BX709408
14	93	9.8	808 29	CC508168	CC508168 CH240.350
15	91.5	9.6	506 13	BU956000	BU956000 HM12802r
16	90.5	9.5	788 14	CK000102	CK000102 AGENCOURT
17	90.5	9.5	922 13	BX355834	BX355834 BX355834
18	90.5	9.5	985 12	BM460288	BM460288 AGENCOURT
19	90.5	9.5	1024 12	BM919028	BM919028 AGENCOURT
20	90	9.5	611 13	BQ869292	BQ869292 Q869292
21	89.5	9.5	932 10	BE536333	BE536333 601062531
22	89.5	9.4	673 13	BU345361	BU345361 604171455
23	89.5	9.4	823 14	CF831057	CF831057 UCCCR01.0
24	89.5	9.4	673 13	BU345361	BU345361 604171455
25	88.5	9.3	563 10	BF490152	BF490152 AT76450.5
26	88.5	9.3	632 14	CA263424	CA263424 SCLH203
27	88.5	9.3	686 14	CA179879	CA179879 SCCST200
28	88.5	9.3	747 29	AG029081	AG029081 Pan trogl
29	88.5	9.3	943 13	BQ891935	BQ891935 AGENCOURT
30	88	9.3	638 9	AT982044	AT982044 par. PK007
31	88	9.3	644 29	CE207073	CE207073 t19t-gss-
32	88	9.3	701 28	AZ870214	AZ870214 2M0182C10
33	88	9.3	840 29	CG058482	CG058482 PPT180TD
34	88	9.3	850 14	CF289682	CF289682 AGENCOURT
35	87.5	9.2	469 12	BG658667	BG658667 T9ESTRyA3
36	87.5	9.2	714 29	CC955012	CC955012 BOIEB1TR
37	87.5	9.2	855 13	BX843917	BX843917 BX843917
38	87	9.1	617 28	AQ471661	AQ471661 CITBI-EI-
39	87	9.1	635 29	CE798899	CE798899 t19t-gss-
40	87	9.1	789 12	BM049470	BM049470 603623401
41	87	9.1	1096 12	BG398113	BG398113 602440150
42	86.5	9.1	515 28	AQ477698	AQ477698 CITBI-EI-
43	86.5	9.1	656 28	AZ869907	AZ869907 2M0182C07
44	86.5	9.1	750 28	B2597628	B2597628 WRAAO30TR
45	86	9.0	696 13	BQ858845	BQ858845 QGC11011.

ALIGNMENTS

RESULT 1
BX473859
LOCUS
DEFINITION
BX473859
ACCESSION
BX473859
VERSION
BX473859.1 GI:31668103
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 634)

AUTHORS Bahr, A., Lauber, J., Mewes, H.W., Weill, B., Amid, C., Osanger, A.,
Fodor, G., Han, W., and Wiemann, S.
TITLE EST (Bahr, A., Lauber, J., Mewes, H.W., Weill, B., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS

Ingo Isenhardt Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 3' sequence available.

This clone (DKFZ686K13165) is available at the RZPD in Berlin.
Please contact the RZPD: Reesourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, Germany; Email: clone@rzpd.de.

FEATURES

source
1. 634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ686K13165"
/dev_stage="adult"
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cDNA-collection"

ORIGIN

Alignment Scores:
Pred. No.: 1.49e-103 Length: 634
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-195-368-1 (1-177) x BK473859 (1-634)

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21 ArgSerSerTrpLeuLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
105 AGATATCACTCGAAGCTGTGCTCTTTGCTCAATAGTATGTTGCTATTTCTTGTCTCC 164
41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaValGluProCysMetAla 60
165 TTCAGTTGGCTATCTTTATTTTCTCCATTAGAGACTGCTAAGAGCCCTGTATGCT 224
61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
225 AAGTTTGACCATTCCTCCAAATGGCAATGGCATCTTGTGAACCTCTTGCGTGAAT 284
81 LysValSerAspTrpLeuLeuGlnIleLeuGlnAsnGlyLeuTrpLeuIleTyrGlyGln 100
285 AAGGCTGTGAGTGAAGCTGAGATCTTCAAGATGCTTATTTATTTATTTATGCGCA 344
101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValArgLeuTyrLysAsn 120
345 GTGGCTCCCAATGACAACTACATATGATGATGCTTTTGAAGTGGCGCTGTATAAAAAC 404
121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyTyr 140
405 AAGGCAATGATTCACAACTCTTACAAACAAATTCAAAATTCAAAATGTAAGGAGACTTAT 464
141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
465 GAATTCATGTTGGGAGACCATATGATGATGATTCATCACTCTGAGCATCAAGTTCTAAA 524
161 AsnAsnThrTyrTrpGlyTyrIleLeuLeuAlaAsnProGlnPheIleSer 177

Db 525 AATAATACATCTGGGGATTCATTACTAGCAAAATCCCAATCATCTCC 575

RESULT 2

AG182677

LOCUS

AG182677 669 bp DNA linear GSS 09-JAN-2002

DEFINITION

Pan troglodytes DNA, clone: RP43-05502.77, genomic survey

ACCESSION

AG182677.1 GI:16712357

VERSION

GSS.

KEYWORDS

Pan troglodytes (chimpanzee)

SOURCE

Pan troglodytes

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

AUTHORS

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

TITLE

Totoki, Y., Matanabe, H., and Sakaki, Y.

JOURNAL

BAC end sequences of library RP43-43

AUTHORS

Unpublished

TITLE

2 (bases 1 to 669)

JOURNAL

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

AUTHORS

Totoki, Y., Matanabe, H., and Sakaki, Y.

TITLE

Submitted (02-AUG-2001) Asac Fujiyama, The Institute of Physical

JOURNAL

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

AUTHORS

1-7-22 Suehiro-chou, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan

TITLE

(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/)

JOURNAL

Clones are derived from the chimpanzee BAC library RP43-43 This BAC

AUTHORS

end was generated during the Rad process and may have higher chance

TITLE

of clone tracking errors.

JOURNAL

PRIMERS

COMMENT

Sequencing: T7

LIBRARY

Vector : pBac3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI

FEATURES

Location/Qualifiers

SOURCE

1. 669

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Percent Similarity: 95.04% Conservative: 1
Best Local Similarity: 94.21% Mismatches: 6
Query Match: 63.93% Indels: 0
Gaps: 0

US-09-195-368-1 (1-177) x AG182677 (1-669)

57 ProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluPro 76
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77 ProCysValAsnLysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeu 96
318 CTTGTGTAATTAAGGTGCTGACTGGAAGCTGAGATACCTTCAGAAATGCTTATATTTA 377
97 ILeTyrGlyGlnValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValArg 116
378 ATTATAGGCAAGTGGCTCCCAATGCAATCATGATGATGCTCTTTAGAGTGGG 437
117 LeuTyrLysAsnLysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnVal 136
438 CTGTATATAAAACAAAGACATGATACAAACTTCACAAACAAATCTTAAATCCAAATGTA 497

VERSION BY214208.1 GI:26394920
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 REFERENCE Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 1 (bases 1 to 348)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 AUTHORS Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamataka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
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 Ito, M., Kagawa, A., Yasunishi, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shiga, M., Shiga, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL MEDLINE
 PUBMED 12354663
 COMMENT 1246851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suhiro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arikawa, T.,
 Hirozane, T., Imocani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numata, K.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Yagami, M., Waki, K., Watanabe, M., and
 Hayashizaki, Y. Direct Submision
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
 Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES
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 Location/Qualifiers
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ORIGIN

Alignment Scores:

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Best Local Similarity:	52.63%	Mismatches:	40
Query Match:	25.24%	Indels:	4
DB:	13	Gaps:	2

US-09-195-368-1 (1-177) x BY214208 (1-348)

53 ThrAlaLysGluProCysMetAlaLysPheGlyProLeuProSerLysTrpGlnMetAla 72
 10 ACTGCCATCGAGTCCTGATGTTAAGTTGAACATATCTCTCAAAATGGCAGATGACA 69
 73 SerSerGluProProCysValenLysValSerAsp-TrpLysLeuGluLysLeuGlnAs 92
 70 TC-TCCCAAACTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 128
 92 ngLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 110
 129 TGGCAATATTTTAAATTTAGCCCACTGATTTCTGCGATTAAGAAATACATTAAGACAA 188
 110 LAlaProPheGluValAlaLysLeuLysLeuLysLeuLysLeuLysLeuLysLeu 130
 189 GGGCCCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 248
 130 sSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 150
 249 TTTTCAATCTTCCCTATGAGGGGCTTATTAATGCTGATGCTGATGATGATGATGAT 308
 150 uilePheAsnSerGluHisGlnValLeuLysAsnSerThr 163
 309 GAAGTCAACTCTAAAGACCATATTCAGAAACTTAACA 348

RESULT 5
 LOCUS BY326400 334 bp mRNA linear EST 11-DEC-2002
 DEFINITION BY326400 RIKEN full-length enriched, synovial fibroblasts Mus
 accession BY326400
 VERSION BY326400
 KEYWORDS BY326400.1 GI:26316959
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 334)
 AUTHORS Nikaide, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batilov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
 Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Fraser, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, R.M., King, B.L., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maitais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M., Sander A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyrshaw-Boris A., Yang G., Yang I., Yang L., Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komori H., Nakamura M., Sakazume N., Sato K., Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E. and Hayashizaki Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
MEDLINE
PUBMED
22354683
12466851

COMMENT

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url: http://genome.gsc.riken.go.jp/
Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Hirozane T., Imotani K., Ishii Y., Itoh M., Kawai J., Komori H., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Maki K., Matakiki A., Muramatsu M. and Hayashizaki Y. Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vasiliis Aidinis (Biomedical Sciences Research Center "Al. Fleming" Institute of Immunology 14-16 Al. Fleming street 16772 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details

FEATURES

SOURCE

Location/Qualifiers
1..334
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/db_xref="taxon:10090"
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/cell_type="synovial fibroblasts"
/clone_id="RIKEN full-length enriched, synovial fibroblasts"

ORIGIN

Alignment Scores:
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Score: 209.50 Matches: 49
Percent Similarity: 60.42% Conservative: 9
Best Local Similarity: 51.04% Mismatches: 35

Query Match: 22.03% Indels: 3
DB: 13 Gaps: 3

US-09-195-368-1 (1-177) x BY326600 (1-334)

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QY 24 TPPLysLeuTPPLysPheCysSerIleValMetLeuLeu---PheLeuCysSerPheSer 42
DB 111 ---AAGTATGAGCTCTTGTCATGATGAGTGGCTCTTACTGATGATGCTCTGTTTGGGT 167
QY 43 TPPLenIlePheIlePheLeuGlnLeuGlnIleThrAlaLysGluProCysMetAlaLysPhe 62
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RESULT 6

BY326606

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

Okazaki Y., Oono N., Saito R., Suzuki H., Yamana H., Nikiido I., Oono N., Saito R., Suzuki H., Yamana H., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gojobori T., Baldarelli R., Hill D.P., Bule C., Hume D.A., Quackenbush J., Schirml L.M., Kanepin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brad D., Brusic V., Chochoia C., Cordani L.B., Cousins S., Daila E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J., Grimond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maitais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ringwald M., Sander A., Schneider C., Sempke C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyrshaw-Boris A., Yang G., Yang I., Yang L., Yuan Z., Zavoian M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Komori H., Nakamura M., Sakazume N., Sato K., Shiraki T., Maki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E. and Hayashizaki Y.

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

12466851
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URL: http://genome.res.riken.go.jp/

Aizawa, K., Akimura, T., Aikawa, T.,

Hiroyane, T., Imotani, K., Ishii, Y.,

Miyazaki, A., Murata, M., Nakamura, M.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D.,

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Computational Analysis of Full-Length Mouse cDNAs Compared with

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cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in Riken.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences

Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.

Fleming street 16672 Vassil, Greece) whose assistance we gratefully

acknowledge.

Please visit our web site (<http://genome.res.riken.go.jp>) for

further details.

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone_id="L030037A06"

/cell_type="synovial fibroblasts"

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ORIGIN

Alignment Scores:

Pred. No.: 1,63e-13 Length: 328

Score: 198.50 Matches: 47

Percent Similarity: 59.57% Conservative: 9

Best Local Similarity: 50.00% Mismatches: 35

Query Match: 20.87% Indels: 3

DB: 13 Gaps: 3

US-09-195-368-1 (1-177) x BY326606 (1-328)

QY 4 SerHsLengLysMetProLeuSerHsSerArgThrGlnGlyAlaGlnArgSerSer 23

DB 51 AGGCTCATGAGAGAAATGCTTTGAGAGATCAAGTCTCCAAAGGCGACAGAGGCGCAAG 110

QY 24 TrpLysLeuTrpLeuPheCysSerIleValMetLeuLeu---PheLeuCysSerPheSer 42

DB 111 ---AAGCATGGCTTGTGCAATGAGGCGCTGCTTACATGATGTGCTGCTTCTTGGGT 167

QY 43 TrpLeuIlePheLeuPheLeuGlnLeuGlnTrpAlaLysGlnProCysMetLalaLysPhe 62

DB 168 ACACTATCTATCTTCACTCAAG---CCAACTGCCATGAGTCCGATGGTGAAGTTT 224

QY 63 GlyProLeuProSerLysTrpGlnMetAlaSerSerGlnProProCysValaLysLysVal 82

DB 225 GAACATCATCTCCCAAAATGACATGACATCTCCCAACCTCACTGTTGAATACGAA 284

QY 83 SerAspTrpLysLeuGlnIleLeuGlnaGlnGlyLeuTrpLeu 96

DB

285 TCTGATGGAGAGCTGAAATCTGCAAGTGGCACTATTATTA 326

RESULT 7

BY327839

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

house mouse

REFERENCE

AUTHORS

324 bp mRNA linear EST 11-DEC-2002

BY327839 RIKEN full-length enriched, synovial fibroblasts Mus

musculus cDNA clone L030044D24 5', mRNA sequence.

EST.

BY327839.1 GI:26518410

EST.

Mus musculus

house mouse

Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base 1 to 324)

Oikazaki, Y., Furuno, M., Kasukawa, T., Adachi, T., Bono, H., Kond, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamazaki, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schombach, C., Golobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

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Batalov, S., Beisel, K.W., Blake, J.A., Bradt, P., Brusio, V.,

Chothia, C., Cordan, L.E., Cousins, S., Datta, E., Drigani, T.A.,

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Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Zimin, P.,

Hayakawa, N., Hirozane-Kishikawa, T., Ito, K., Kawai, J., Kato, K.,

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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shingawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

JOURNAL

MEDLINE

PUBMED

COMMENT

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Aizawa, K., Akimura, T., Aikawa, T.,

Hiroyane, T., Imotani, K., Ishii, Y.,

Miyazaki, A., Murata, M., Nakamura, M.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D.,

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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

FEATURES

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Location/Qualifiers
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ORIGIN

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DB:	13
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Matches:	45
Conservative:	9
Mismatches:	35
Indels:	3
Gaps:	3

QY	4	SeRH1LdENGLyAmneCProLeuSerH1SerAgtHrInglYAlaInYAgSerSer	23
	
Db	51	AGCCTATGAGGAAATGCTTTGGAGAAATCAAGTCTCAAAAGGAGAGAGTCAAG	110
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QY	43	TriPheIleAPheIlePheUenIeuLeuInHrAlaYsgIuProCysMetalAlaYsPe	62
	
Db	168	ACACTATCTATATCTTCACTCAAG--CCAACTGCATCGAGTCTCTCAAGCTTAAGTTT	224
QY	63	GlyProLeuProSerIleYTriPglImeAlaSerGluProProCysValaenYsVal	82
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QY	83	SerAspTriPlyLeuInglIleUenInaInglYLeuYr	95
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RESULT 8			
AG043514			
LOCUS			
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ACCESSION	Pan.trog1odyes DNA, clone: PTB-021N15.R,		genomic survey sequence.
VERSION	AG043514.1		
KEYWORDS	GI:16572239		
SOURCE	GSS.		
	Pan. troglodytes (chimpanzee)		

and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimbbs@gsc.riken.go.jp, URL: <http://hsp.gsc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170). Clones are derived from the chimpanzee BAC library FTB. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

FEATURES

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Location/Qualifiers
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ORIGIN

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Best Local Similarity:	80.85%
Query Match:	20/24
DB:	29
Gaps:	1

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Qy 30 CysSerIleValMetLeuIleuPheIleuGlySerPheSerTrrpLeuIlePheIleLeu 49
      |:::|
Db 95 TGCTCAATGATTAAGTGTATTCTTTGTCCTCTCAAGTGGCTTAATCTTATTTTCTC 154

Qy 50 GlnLeuGlnThrAlaIysGlu 56
      |:::|
Db 155 CAATTAGAGCTAAGAGGCCAA 175

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RESULT	9
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DEFINITION	CG977950 114 bp DNA linear GSS 15-DEC-2003 CH240_168010.TV CHORI-240 Bos taurus genomic clone CH240_168010, genomic survey sequence.
ACCESSION	CG977950
VERSION	CG977950.1 GI:3903729
KEYWORDS	GSS.
SOURCE	Bos taurus (cow)
ORGANISM	Bos taurus

Clones are derived from the bovine BAC library CHORI-240
 (<http://www.chori.org/bacpac/bovine240.htm>).
 Bases shown have phred quality value equal to or higher than 20.
 For BAC library availability, please contact Pieter de Jong
 (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/ordering/information.htm>).

This work was undertaken as part of the International Bovine BAC
 Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e
 Biotecnologia with financing from Conselho Nacional de
 Desenvolvimento Científico e Tecnológico (CNPq), Brazil
 Plate: 168 row: J column: 10
 Seq primer: T7
 Class: BAC ends

High quality sequence stop: 114.

FEATURES

source

Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	Length:	Mismatches:	Conservative:	Mismatches:
Score:	0.000206	114	19	
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Query Match:	12.308		0	
DB:	29	Gaps:	0	

US-09-195-368-1 (1-177) x CG977950 (1-114)

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RESULT 10
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 LOCUS BU294618 60303521F1 CSEQCHN55 Gallus gallus cDNA clone CHEST58216 5', mRNA
 DEFINITION

ACCESSION BU294618 GI:25744254
 VERSION BU294618
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE
 AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A., and Hubbard, S.C.

TITLE A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 MEDLINE 22355534
 PUBMED 12445392

COMMENT Contact: Simon Hubbard
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 (UMIST)

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 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source

Location/Qualifiers
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 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer.
 Following this, first strand reaction, double-stranded cDNA
 was blunted, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Mismatches:	Conservative:	Mismatches:
Score:	0.0238	727	38	
Percent Similarity:	110.00		23	
Best Local Similarity:	48.03%		46	
Query Match:	29.928		20	
DB:	11.57%	Gaps:	6	

US-09-195-368-1 (1-177) x BU294618 (1-727)

QY 62 PheGlyProleuProserIySTpGInMeAlaserSerGIuProProCyValnslyVal 81
 DB 184 TTCTCCCAAGTG---CTGAAGTGG---ATGACGACGAGCTACGCCCAAGCAGCAGCTTG 237
 QY 82 ValSer-----AspTrpIySleuGluIleuGlnAsnGlyLeuTyrtleuTyrgly 99
 DB 238 ATATCTTACCATGAGGAGGAGCTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 297
 QY 100 GlnValAlaProAsnAlaAsnTyrsAspValAlaProPheGlnValArgIleuTyrr--- 118
 DB 298 CAAGTACGCTTGCGACCAAGCGGCGGCTTGGCGGCCCTTCAACCTCATATTTATTGG 357
 QY 119 -----LysAsnLysAspMetIleGlnIleu 127
 DB 358 TACCTCCCATGAGAGGAGCGGCTCTGATGAAAGGAGCTTGAACGACGACGACCTCC 417
 QY 128 ThrAsnLysSerIySleGlnAsnVal-----GlyGlyThrTyrgluIleuHisValGly 145
 DB 418 ACGGCTCTGTGAGGCTCAGTCATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 477
 QY 146 AspThr-----IleAspIleuIlePheAsnSerGluHisGlnValLeuLysAsnThr 163
 DB 478 GACATGCTTTTGTATGATGAGGAGCTCAACGACGAGTGAACGTAACCTGGCAACCC 537
 QY 164 TyrtPglyIleIleleuIleu 170
 DB 538 TACTTGGATGATGTTACAGCTG 558

RESULT 11
 BU373331 731 bp mRNA linear EST 28-NOV-2002
 LOCUS BU373331 603589056F1 CSEQCHN74 Gallus gallus cDNA clone CHEST549p13 5', mRNA
 DEFINITION

sequence.
 ACCESSION BU373331 GI:25881332
 VERSION BU373331.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 731)
 Boudreau, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 CURT. Biol. 12 (22), 1965-1969 (2002)
 JOURNAL MEDLINE 22335534
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 10D, UK
 Tel: 0161208930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

source
 1..731
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton Line 151"
 /db_xref="taxon:9031"
 /clone="CH261-17B4"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="MDH103"
 /clone_lib="CSECHN74"
 /note="Organ: Kidney + adrenal; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.: 0.024 Length: 731
 Score: 110.00 Matches: 38
 Percent Similarity: 48.03% Conservative: 23
 Best Local Similarity: 29.92% Mismatches: 46
 Query Match: 11.57% Indels: 20
 DB: 13 Gaps: 6

US-09-195-368-1 (1-177) x BU373331 (1-731)

Cy 62 PhegiyProlenProserlyTgplmMelaSerSerupPropocysValaLys 81
 Db 186 TTTCTCCCAAGTG--CTGAAGTGG--ATGACGACGACTGAGCCCAACAGCAGCTTG 239
 Cy 82 ValSer-----AspTrpLysLeuGluLeuGlnAnsglyLeuTYLeuileTYrGly 99
 Db 240 ATATCTACCATGAGGGAGAGCTGAGGTGAAGAAAGCAGGCTCTACTACATCTCA 299
 Cy 100 GlnValAlaProAlaAlaAsnTYrAspValAlaPheGluValAlaGlyLeuTY--- 118
 Db 300 CAAGTACCTTGTGACCAAGCGGCGCTTGGGCGCATTCACCCCTCTATATTATTG 359

Cy 119 -----LysAnlySappMetIleGlnThreu 127
 Db 360 TACTCCCATGAGAGACCGGCTCTGTATGAAAGACTTGACACGACAGCACTCC 419
 Cy 128 ThrAnlySerLysIleGlnAnVal-----GlyTYrTrpTYrGluLeuHleValGly 145
 Db 420 ACGGCTCTGTGAGCTCATGCTCCATCCGAGAGCGGCTGTCTTGAGCTCGGCGAGGC 479
 Cy 146 AspThr-----IleAspLeuIlePheAnSerGluHleGlnValLeuLysAnbnThr 163
 Db 480 GACATGCTCTTGTCAATGTCAGCGACGACGACGACGACGACGACCTGGCAACAC 539
 Cy 164 TYTTPGlyIleIleLeuLeu 170
 Db 540 TACTTGGCATGTCAAGCTG 560

RESULT 12

CC250868

LOCUS CH261-17B4 Sp6.1 CH261 Gallus gallus genomic clone CH261-17B4,

DEFINITION genomic survey sequence.

ACCESSION CC250868

VERSION CC250868.1 GI:30587618

KEYWORDS GSS.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 1514)

AUTHORS Kremutzki, C., Higgibotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.

TITLE Gallus gallus BAC End Reads

JOURNAL Unpublished (2003)

COMMENT Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submisions@wustl.edu

Insert Length: 182000 Std Error: 0.00

Seq primer: Sp6 ATTAGGTGACACTATAG

Class: BAC ends

High quality sequence start: 326

High quality sequence stop: 920.

Location/Qualifiers

1..1514
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-17B4"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTRABAC2.1; Site 1: EcoRI; Site 2: EcoRI; CH261 Female Chicken library - For library and clone ordering information: <http://www.chori.org/bacpac>"

ORIGIN

Alignment Scores:

Pred. No.: 3.49 Length: 1514
 Score: 96.00 Matches: 45
 Percent Similarity: 37.95% Conservative: 18
 Best Local Similarity: 27.11% Mismatches: 54
 Query Match: 10.09% Indels: 50
 DB: 28 Gaps: 7

US-09-195-368-1 (1-177) x CC250868 (1-1514)

Cy 6 LeuGluAsnMetProlenSerHisSerArgThngInglyAla---GlnArgSerSerTrp 24
 Db 674 TTGAACACTTTTCTCTCTACACACAGTGAATTAAGGCTCTTGATGATTTCCAGTTGG 733
 Cy 25 LysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSerPheSerTrpLeu 44

TITLE
JOURNAL
COMMENT

Dailymp, B.P. and Tellam, R.
Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
Unpublished (2003)
Other GSSs: CH240_350K10.TARBA13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4B6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bccsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Science Centre, Canada.
Plate: 350 row: K column: 10
Seq primer: T7
Class: BAC ends.

FEATURES

source
Location/Qualifiers
1. 808
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_350K10"
/sex="male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull U Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Alignment Scores:

Pred. No.: 3.09 Length: 808
Score: 93.00 Matches: 41
Percent Similarity: 38.46% Conservative: 24
Best Local Similarity: 24.26% Mismatches: 36
Query Match: 9.78% Indels: 68
DB: 29 Gaps: 10

US-09-195-368-1 (1-177) x CCS08168 (1-808)

QY 9 MetProLeuSerHisSerArgThrGln----- 17
DB 344 CTCCTCTTCTTCTTTCAGAGAACCTGGGACCTCTCTTAAGGGGATGAGTGTCT 403
QY 18 -----GTAAGlnArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeu 35
DB 404 GCGTGGGCTGTAGAGGGGAGGAGCTGCAG-----TGCTCC----- 439
QY 36 LeuPheLeuCysSerTrpLeuIlePheIlePheLeuGlnLeuGlnThr----- 53
DB 440 -----TCCGTGAGCTGGCTGTGCTGTGCACTTCTGCTCTCCAGCTCTTT 487
QY 54 -----AAlaYSgLuPProCysMetAlaLysPheGly----- 63
DB 488 CTCCTGATCTCTCTGGGGGTTTCAGAGAGAGCTGAAGTGGAGTTCTGGGGAATGAC 547
QY 64 -----ProLeuProSerLysTrp-----GlnMet 71
DB 548 TTTTACCTTTGTGGGTGAGGACACCTCTGCTGTGAGAGGTGAGAAAGGGGAGAC 607
QY 72 AlaSerSerGluProPro-----CysValAsnLysValSerAspTrpLysLeuGln 86
DB 608 TCAAGTGGGAGCACTGAGGTGAGTGTGAGGCAACTTGAACCTTGG----- 658
QY 89 IleLeuGlnAsnGlyLeuTrpLeuIleTrpGlyGlnValAlaProAsnAlaAsnTrpAsn 108

DB 659 -----GGCTGAAGGCTTCTGGTGGTACCGGCCCC----- 691
QY 109 AspValAlaProPheGluValArgLeuTrpLysAsnLysAspMetIleGlnTrpLeuTrp 128
DB 692 -----TCCCACTAGAGCACCGAGCTTAAAGATCAACACAGCTGTGACTCATTTGTT 745

QY 129 AsnLysSerLysIleGlnAsnValGly 137
DB 746 -----GGAGAAATTCAGTCAATGGGC 766

RESULT 15

BU996000 506 bp mRNA linear EST 23-OCT-2002
LOCUS HM12B02 HM Hordeum vulgare subsp. vulgare cDNA clone HM12B02
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BU996000
KEYWORDS BU996000.1 GI:24272983
SOURCE EST.
Organism Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 506)
Zhang, H., Weschke, W., Michael, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 506 Std Error: 0.00
Plate: 12 row: B column: 2
Seq primer: M13rev.

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source
Location/Qualifiers
1. 506
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultiivar="barke"
/sub_species="vulgare"
/db_xref="GABI:255878"
/db_xref="taxon:112509"
/clone="HM12B02"
/tissue type="male inflorescences"
/dev stage="male inflorescences (approx. 2 mm in size),
green anther stage"
/lab_host="XU10-Gold"
/clone_lib="HM"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

ORIGIN

Alignment Scores:

Pred. No.: 2.3 Length: 506
Score: 91.50 Matches: 36
Percent Similarity: 45.13% Conservative: 15
Best Local Similarity: 31.86% Mismatches: 54
Query Match: 9.62% Indels: 8
DB: 13 Gaps: 3

US-09-195-368-1 (1-177) x BU996000 (1-506)

QY 1 MetCysLeuSerHisLeuGluAsn-MetProLeuSerHisSerArgThrGlnGlyAlaG1 20
:::||||| ||| ||||| :::: ||||| ::::

```

Db      23 CTCTGCTCTCTACATAGAGAAAACAGTTCTCTCTCATACAGAAAGATGGGTTCA-- 80
Qy      20 nArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCys9e 40
Db      81 ----ACACCGCTCAGGCTCATGCTTGTCTCTCCGCTCATGCTACTCATGCACTGCAC 136
Qy      40 rPheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAla--LysGlnProCysMe 59
Db      137 TCACCGCGGAGCAGCCGAGAGCTTTCTTCAGACACCGAGCGGCGGTGAAGACGTGTGCGGT 196
Qy      59 fAlaIys-----PheGlyProLeuProSerLysTrpGlnMetAlaSerSerGI 75
Db      197 GGCCTAGGCTTCGACCGGAGGAGCGGCGCTCAGGCGCCACCTGAGAGTTCGCTCTCCGA 256
Qy      75 uProProCysValAsnLysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTy 95
Db      257 GAGCGACTGACAGCGGATCCAGGCGACGCGGCGCTGCTCCGCACTGAACGCGCGCTGCT 316
Qy      95 rLeuIleTyrglyGlnValAlaProAsnAlaAsnTy 107
Db      317 GCTGTGCGGCGGTGCTGCGCATGTAACGCTTACTAC 353

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Search completed: April 7, 2004, 19:35:47
 Job time : 2440.23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2004, 15:53:26 ; Search time 314.795 Seconds
(without alignments)
2388.639 Million cell updates/sec

Title: US-09-195-368-1

Perfect score: 951
Sequence: 1 MCLSHENNPPLSHRTQAGQ.....VLKNTYGIILANPQIS 177

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n model -DRV=xld
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-DB=N Geneseg 290404 -QFMT=fstep -SUPFL=eng -MINMATCH=0.1 -LOOCL=0
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09195368 @CGN 1.1 886 @runat_07042004_061637_2588 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOUTRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseg 290404:*

1: geneseg1980s:*\n2: geneseg1990s:*\n3: geneseg2000s:*\n4: geneseg2001as:*\n5: geneseg2001bs:*\n6: geneseg2002s:*\n7: geneseg2003as:*\n8: geneseg2003bs:*\n9: geneseg2003cs:*\n10: geneseg2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	534	7	ACC57580 Polynucle
2	951	100.0	534	7	ACC57909 Human GIT
3	951	100.0	534	9	ADCS5221 Human CDN
4	951	100.0	1809	2	AAV19195 Human end
5	951	100.0	1849	3	AAAT74936 CDNA end
6	951	100.0	1849	3	AAZ57314 Human end
7	951	100.0	1849	8	ADAI1463 Human end
8	951	100.0	1849	9	ADCO1857 Human CDN

9	951	100.0	1964	2	AA559844	AA559844	CDNA	seqn
10	951	100.0	1964	2	AA87726	AA87726	Human	PRO
11	951	100.0	1964	4	AA65435	AA65435	Clone	PRO
12	951	100.0	1964	4	AA30051	AA30051	Human	CDN
13	951	100.0	1964	4	AA97374	AA97374	Human	ang
14	951	100.0	1964	4	AA685945	AA685945	Native	se
15	951	100.0	1964	4	AA90563	AA90563	Human	PRO
16	951	100.0	1964	5	ABK28562	ABK28562	Human	DNA
17	814	85.6	1527	5	AA50614	AA50614	DNA	encod
18	814	85.6	1527	5	AA581613	AA581613	DNA	encod
19	281	29.5	162	4	AAK3619	AAK3619	Human	bon
20	170	17.9	397	4	AAK30610	AAK30610	Human	bon
21	107	11.3	60	6	ABN41382	ABN41382	Human	sp1
22	92	9.7	50	6	ABZ02741	ABZ02741	Human	leu
23	86.5	9.1	455	8	ACH41523	ACH41523	Human	foe
24	86	9.0	320	8	ABN18154	ABN18154	Human	orf
25	86	9.0	2637	6	ABL40958	ABL40958	Human	tra
26	86	9.0	58708	4	AAK64739	AAK64739	Human	imm
27	85.5	9.0	3515	6	AAD31199	AAD31199	Human	WKL
28	85.5	9.0	3515	6	AAD31200	AAD31200	Human	WKL
29	85.5	9.0	3650	4	AA158154	AA158154	Human	pol
30	85.5	9.0	3650	8	ADBA48120	ADBA48120	Novel	hum
31	85.5	9.0	3912	4	AA160197	AA160197	Human	pol
32	85.5	9.0	15690	6	ABK15000	ABK15000	Canine	di
33	84.5	8.9	1008	6	AB198960	AB198960	Canine	di
34	84.5	8.9	1727	4	AA560941	AA560941	Human	can
35	84.5	8.9	1797	6	ABN65564	ABN65564	Streptococ	
36	84.5	8.9	2641	6	ABZ82536	ABZ82536	Human	sec
37	84.5	8.9	3665	9	ADC90678	ADC90678	E. faeciu	
38	84.5	8.9	4042	5	AA583774	AA583774	DNA	encod
39	84.5	8.9	15690	6	ABK15038	ABK15038	Canine	di
40	84.5	8.9	18826	6	ABK15039	ABK15039	Canine	di
41	84.5	8.9	110000	6	ABN71527_07	ABN71527_07	Continuation	(8 of
42	84	8.8	569	9	ADD34676	ADD34676	Mouse	mit
43	84	8.8	100301	6	ABO88176	ABO88176	Human	ost
44	83	8.7	10697	4	AAK93607	AAK93607	Human	imm
45	83	8.7	10697	5	ABA21005	ABA21005	Human	ner

ALIGNMENTS

RESULT 1
ACC57580 standard; DNA; 534 BP.
ACC57580;
28-JUL-2003 (first entry)
Polynucleotide encoding tumour necrosis factor superfamily member.
Human; RANKL; tumour necrosis factor; osteopathic; bone; gene; ds.
Homo sapiens.
WO2003033663-A2.
24-APR-2003.
15-OCT-2002; 2002WO-US033022.
15-OCT-2001; 2001US-0329393P.
15-OCT-2001; 2001US-0329393P.
(BARN-) BARNES-JEWISH HOSPITAL.
Iam J, Ross PF, Teitelbaum SL;
WPI; 2003-430346/40.
New RANKL mimic comprising a core, and at least one external loop, useful for enhancing processes of bone formation or inhibiting bone resorption, thus providing treatments for disease or condition characterized by loss of bone mass.

XX PS Disclosure, Page 58, 78pp, English.

CC The present sequence is that of a polynucleotide encoding a non-RANKL member of the tumour necrosis factor (TNF) superfamily. The invention provides non-naturally-occurring proteins that contain one or more of the external surface loops of RANKL (see ABR42066-70) in combination with a heterologous protein core obtained from a non-RANKL member of the TNF superfamily. Also provided are polynucleotides encoding such proteins. The proteins bind to RANK, acting as mimics of RANKL. They can be used to enhance bone formation by either inhibiting bone resorption or inducing osteogenesis, thus providing treatment for diseases or conditions characterised by loss of bone mass

CC Sequence 534 BP, 161 A, 107 C, 104 G, 162 T, 0 U, 0 Other;

US-09-195-368-1 (1-177) x ACC57580 (1-534)

Alignment Scores:

Pred. No.:	2,16e-100	Length:	534
Score:	951.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 1 ATGTGTTGAGCCACTTGGAANAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 60
 21 ArgSerSerTrpLeuTrpLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 61 AGATCATCTCGAAGCTGGAGCTCTTTGCTCAATAGATTAGTTCCTTATTTCTTGCTCC 120
 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
 121 TTCAGTTGGCTAATCTTATTTCTCCAAATTAGAGCTGAAGAGCCCTGATGGCT 180
 61 LysPheGlyProLeuProSerSerIleTrpGlnMetAlaSerSerGluProCysValAsn 80
 181 AAGTTGGAGCATTACCTCCAAATGGAATGGCAATGTCATCTTGAACCTCTTGATGGTAA 240
 81 LysValSerAspTrpLeuGlnGlnLeuGlnAsnGlyLeuIleLeuIleTyrGlyGln 100
 241 AAGGTGTGAGTGAAGCTGGAATGACTTCAAGATGCTTATTAATTTATGAGCCAA 300
 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
 301 GTGGCTCCCAATGCAAACTGACATGATGAGCTCTTTGAGTGCGGCTGATATAAAAC 360
 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
 361 AAGACATGATCAAACTCTTAACAAACAATCTAAATCCAAATGTAAGAGGAGGACTTAT 420
 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 421 GAATTCAGATGTGGGAGACACCATAGACTTGATTTCAACTCTGAGCACAAGATCTTAAA 480
 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 481 AATAATACATACGGGGTATCATTTTACTAGCAAAATCCCAATTCATCTCC 531

RESULT 2
 ACC57909
 ID ACC57909 standard, cDNA, 534 BP.
 AC ACC57909;
 XX 11-AUG-2003 (first entry)
 DT Human GITRL polynucleotide.
 XX Human GITRL polynucleotide.
 KW Human; GITRL; tumour necrosis factor; ligand; cytostatic;

KW immunomodulator; osteopathic; gene; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..534

FT /tag= a

FT /product= "Human GITRL"

XX WC003040307-A2.

XX 15-MAY-2003.

XX 25-JUL-2002; 2002WC-US023782.

XX 27-JUL-2001; 2001US-030783BP.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Hilbert DH, Rosen CA;

XX WPI, 2003-430659/40.

XX P-PSDB; ABR42323.

XX New heteromultimeric complex having a first polypeptide member of the

PT tumor necrosis factor (TNF) ligand family, and a second different member

PT of TNF ligand family, useful for treating cancer, osteoporosis or an

PT autoimmune disease.

XX PS Disclosure, Page 382, 388pp, English.

XX The present sequence is that of a polynucleotide encoding human GITRL.

CC The invention relates to compositions comprising heterotrimeric complexes

CC of tumour necrosis factor (TNF) ligand family members, and their use in

CC the detection, prevention and treatment of disease. In preferred

CC embodiments, the heterotrimeric complex comprises full-length or

CC extracellular portions of other TNF ligand family members. The

CC heterotrimeric complexes of the invention are useful for treating an

CC autoimmune disease, cancer or osteoporosis, and particularly for

CC inhibiting cancer cell proliferation, increasing B cell proliferation, or

CC inducing apoptosis of T cells

XX SQ Sequence 534 BP, 161 A, 107 C, 104 G, 162 T, 0 U, 0 Other;

US-09-195-368-1 (1-177) x ACC57909 (1-534)

Alignment Scores:

Pred. No.:	2,16e-100	Length:	534
Score:	951.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	7	Gaps:	0

1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 1 ATGTGTTGAGCCACTTGGAANAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 60
 21 ArgSerSerTrpLeuTrpLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 61 AGATCATCTCGAAGCTGGAGCTCTTTGCTCAATAGATTAGTTCCTTATTTCTTGCTCC 120
 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
 121 TTCAGTTGGCTAATCTTATTTCTCCAAATTAGAGCTGAAGAGCCCTGATGGCT 180
 61 LysPheGlyProLeuProSerSerIleTrpGlnMetAlaSerSerGluProCysValAsn 80
 181 AAGTTGGAGCATTACCTCCAAATGGAATGGCAATGTCATCTTGAACCTCTTGATGGTAA 240
 81 LysValSerAspTrpLeuGlnGlnLeuGlnAsnGlyLeuIleLeuIleTyrGlyGln 100

Accession	Protein	Length
D8	AAAGTGTGACCTGCAAGAGCTGGAGAGTACTTCAGATGGCTTAATTAATTATTATGAGCAA	300
D24	AAAGTGTGACCTGCAAGAGCTGGAGAGTACTTCAGATGGCTTAATTAATTATTATGAGCAA	300
QY	ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrTyrosAsn	120
D8	GTGAGCTCCCAATGCAACATCACTAGTGTAGCTCTTTTGAGAGTGGCTGTATATTAATAAC	360
QY	LysAspMetIleGlnThrLeuThrAsnLysSerTyrIleGlnAsnValGlyThrTyr	140
D8	AAAGACATGTATCAAACTCTAACAAACAATCTATAATCCAAATAGTGAAGAGGACTTAT	420
QY	GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys	160
D8	GAATTGAGTTTGAGGACACCAATAGACTTGATTAATTCACCTCGACACATCAGAGTCTATAAA	480
QY	AspAsnThrTyrTyrGlyIleIleLeuLeuAlaAsnProGlnPheIleSer	177
D8	AAATATATCATCTGGGATATCATTTTACTACGAAATCCCAATTCATCATCTCC	531

RESULT 3
 ID ADC35221
 ADC35221 standard; cDNA; 534 BP.
 AC ADC35221;
 DT 18-DEC-2003 (first entry)
 DE Human cDNA encoding TNF ligand family member #20.
 KW sb; gene; human; tumour necrosis factor; TNF ligand; endokine alpha;
 KW excessive bone resorption disorder; osteoporosis; Paget's disease;
 KW arterial calcification.
 XX
 OS Homo sapiens.
 XX
 PN US2003100074-A1.
 PD 29-MAY-2003.
 PF 15-AUG-2002; 2002US-00218547.
 PR 16-AUG-2001; 2001US-0312542P.
 PR 30-OCT-2001; 2001US-0330761P.
 XX
 PA (YUGG/) YU G.
 PA (NIJ/) NI J.
 PA (ROSE/) ROSEN C A.
 PA (NARD/) NARDELLI B.
 XX
 PI YU G, NI J, ROSEN CA, NARDELLI B;
 DR WPI: 2003-696072/66.
 DR P-PsDB: ADC35222.
 XX
 PT New Endokine alpha gene useful for preparing a composition for treating a
 PT disease associated with excessive or insufficient bone resorption e.g.,
 PT osteoporosis, Paget's disease or arterial calcification.
 XX
 PS Disclosure; SEQ ID NO 39; 145bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule encoding a
 CC tumour necrosis factor family ligand. A composition comprising the
 CC isolated antibody or its fragment is used for treating an individual in
 CC need of decreased level of endokine alpha activity. The endokine alpha
 CC polypeptide present in a heterotrimeric complex is used for treating an
 CC individual having a disorder associated with excessive bone resorption,
 CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
 CC individual having a disorder associated with insufficient bone resorption
 CC comprises administering an endokine alpha antagonist, which is the
 CC antibody that binds specifically to endokine alpha polypeptide. The
 CC present sequence represents a cDNA encoding a tumour necrosis factor
 CC family ligand.
 XX
 SEQ Sequence 534 BP; 161 A; 107 C; 104 G; 162 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	2.16e-100
Score:	534
Percent Similarity:	95.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
Length:	534
Matches:	177
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-195-368-1 (1-177) x ADC35221 (1-534)

Oy			I MetCysLeuSerHisIleuGlnAsnMetProIleuSerHisSerArgThrGlnGlyAlaGln	20
Db			1 ATGTGGTTTAGCCACTGGAAATATAGCTTAAAGCCATTCAAGAACCTCAAAGAGCTCG	60
Oy			21 ArgSerSerTriplyshenrPheuphEcYsserIleValMelLeuLeuphEucYsser	40
Db			61 AGATCATCTCGAAGCTGGTGCTCTTTGGCTCAATAGTATGCTGATTTCTTGCTCC	120
Oy			41 PheSerTripleuIllePheIllePheLeuGlnLeuGluThraIalylsgluproCYsMerAla	60
Db			121 TTGAAGTTGGCTATCTTTATTTTTTCCTCCATTAGAGACTGTGAAGAGCCCTGTATGGCT	180
Oy			61 LysPheGlyProIeuProserLysTrpGlnMetAlaserSerGluProproCYsValAsn	80
Db			181 AAGTTTGACCATTAACCTCCAAATGGCAATGGCATCTTCTGAACCTCTTGCTGAT	240
Oy			81 LysValSerAspTriplyshenrLeuGlnIleLeuGlnaengilyLeuTyrlleTyrglyGln	100
Db			241 AAGGTGTCTGACTGGAAGCTGGAGATACTTCAAGATGGCTTATTTTAATTATGGCCAA	300
Oy			101 ValAlaProAsnAlasnrTyrsAspValAlaProPheGlyValArgLeuTylyAsn	120
Db			301 GTGGCTCCCAATGCACAATCAATATGATGACTCTTTTGAGGTCGCGCTGTATAAAAAC	360
Oy			121 LysAspMerillegInthrPheThrAsnLYsserLYsIlegInaenValglyThrTYr	140
Db			361 AAAGACATGATACAACTTAACCTTAACAACAATCTTAATAATCCAATGTAGAGAGCACTAT	420
Oy			141 GluLeuHISvalglyAspThrIleaspLeuIllePheasnSerGIuHISglnValLeuLYs	160
Db			421 GAATTGCATGTTGGAGCACACCATAGACTTGATATTCAACTCTGAGCATCAAGGTTCTAAA	480
Oy			161 AsaAsnthrThrTrpGlyIlelleLeuLeuAlaasnProGlnpheIleser	177
Db			481 AATATATCATACTGGGGTATCATTTTACTACGAATATCCCACATTCATCTCC	521

RESULT 4			
ID	AAV19195		
AC	AAV19195 standard; cDNA; 1809 BP.		
XX	AAV19195;		
DT	28-AUG-1998 (first entry)		
DE	Human endokine-alpha CDNA.		
KM	Endokine-alpha; cytokine; tumour necrosis factor; human;		
KW	immunomodulation; infection; cell proliferation; angiogenesis; tumour;		
KM	metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;		
XX	diagnosis; therapy; de; ss.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	CDS	53..562	
PN		/+tag= a	
PD	MO9807880-A1.		
XX	26-FEB-1998.		
EF	16-AUG-1996; 96WO-US013282.		

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XX 16-AUG-1996; 96MO-US013282.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Yu G, Ni J, Rosen CA;
XX WPI; 1998-169182/15.
XX P-PSDB; AAM37847.
XX Nucleic acid encoding human endokine-alpha - useful for diagnosis and
XX treatment of tumour necrosis factor-related diseases.
XX Claim 1; Fig 1A-B; 78pp; English.
XX This isolated nucleic acid, deposited as ATCC 97640, codes for human
XX endokine-alpha (see AAM37847), a novel member of the tumour necrosis
XX factor (TNF) family of cytokines. It was isolated from a cDNA library
XX established from human striatum. Expressed sequence tags corresponding to
XX a portion of the endokine-alpha cDNA were also found in several
XX endothelial libraries and a foetal liver library. Isolation of the
XX nucleic acid allows production of recombinant endokine-alpha in
XX transformed host cells. Endokine-alpha may be involved in disorders of
XX immunomodulation, infection, cell proliferation, angiogenesis, tumour
XX metastasis, apoptosis, sepsis and endotoxaemia, and may be useful for
XX treating melanoma and sarcoma. A claimed diagnostic method comprises
XX assaying endokine-alpha gene expression as a means of detecting a TNF-
XX related disorder. Fragments of endokine-alpha nucleic acids can be used
XX as probes, e.g. for fluorescent in situ hybridisation, for identifying
XX genomic or other related sequences and in chromosome identification.
XX Sequence 1809 BP; 549 A; 355 C; 351 G; 554 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1 25e-99 Length: 1809
XX Score: 951.00 Matches: 177
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 2 Gaps: 0
XX
XX US-09-195-368-1 (1-177) x AAV19195 (1-1809)
XX
XX 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
XX 29 ATGCTTTGACCCCACTTGGAATAATATGCTTTAAGCATTCAGAACTCAAGAGCTCAG 88
XX 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
XX 89 AGATCATCTCGAAGCTGTGCTCTTTGCTCAATAGTATGTTGCTATTCTTGTCTCC 148
XX 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGlnProCysMetAla 60
XX 149 TTCAGTTGCTCAATCTTATTTTCTCCAAATTAGACTGCTAAGAGCCTGATGCT 208
XX 61 LysPheGlyProLeuProSerIleTrpGlnMetLysSerGlnProProCysValAsn 80
XX 209 AAGTTTGAACATTAACCTCAAAATGGCAATGGCAATGCTCTTGTGCTGAT 268
XX 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTrpGlyGln 100
XX 269 AAGGTGCTGACTGGAAGCTGGAAGTACTTCAGAAATGGCTTAATTAAATTATGCGCAA 328
XX
XX 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGluValaGlnLeuTrpLysAsn 120
XX 329 GTGGCTCCCAATGCAAACTACAAATGATGACTCTTGTGGGGCGCGCTATAAAAAC 388
XX 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValaGlyGlyThrTrp 140
XX 389 AAAAGCATGATACAAACTCTTAACAAACAAATCTAAATCCAAATGTAGAGGAGGACTTAT 448
XX 141 GluLeuHisValaGlyAspThrTrpLeuPheLeuLeuPheAsnSerGlnHisGlnValLeuLys 160

```

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DB 449 GAATTCATGTTGGGGAACCATTAAGTGAATTCGAAGTCAAGCTTCTAAAA 508
XX
XX 161 AsnAsnThrTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
XX 509 AATAATACCTACTGGGATATCATTTTACTGCGAAATCCCAATCATCATCTCC 559
XX
XX RESULT 5
XX AAM74936
XX ID AAA74936 standard; cDNA; 1849 BP.
XX
XX AAA74936;
XX
XX 02-JAN-2001 (first entry)
XX
XX cDNA encoding a human endokine-alpha polypeptide.
XX
XX Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;
XX chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
XX autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
XX acute inflammation; acute allograft rejection; graft versus host disease;
XX transplant rejection; foetal resorption; faecal peritonitis;
XX bowel disease; sepsis; leukaemia; chronic hypergammaglobulinemia;
XX polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
XX chronic active hepatitis; myasthenia gravis; psoriasis; vitiligo;
XX Steven-Johnson syndrome; idiopathic sprue; gluten-sensitive enteropathy;
XX pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
XX discoid lupus; dense deposit disease; endocrine ophthalmopathy;
XX irritable bowel disease; asthma; Grave's disease; sarcoidosis;
XX juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
XX lymphopneumonia; polyarteritis nodosa; Sjogren's syndrome; Behcet's disease;
XX primary myxedema; polyomyositis; mixed connective tissue disease;
XX keratoconjunctivitis sicca; vernal keratoconjunctivitis; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 53..562
XX /*tag= a
XX /product= "endokine-alpha"
XX
XX MO200050620-A2.
XX
XX 31-AUG-2000.
XX
XX 25-FEB-2000; 2000MO-US004722.
XX
XX 26-FEB-1999; 99US-0122099P.
XX 28-MAY-1999; 99US-0136788P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Rosen CA;
XX WPI; 2000-572097/53.
XX P-PSDB; AAB08785.
XX
XX polynucleotide encoding endokine alpha protein, which is a member of
XX tumour necrosis factor useful for treating inflammatory diseases,
XX disorders such as cancer, allergy, diabetes and various neurological
XX disorders.
XX
XX Claim 5; Fig 1; 263pp; English.
XX
XX The present sequence encodes a human endokine-alpha polypeptide. The
XX polypeptide is a cytokine which is similar to tumour necrosis factor
XX (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
XX treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
XX autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
XX inflammation, acute inflammation, acute allograft rejection, graft versus
XX host disease, transplant rejection, foetal resorption, faecal
XX peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
XX hypergammaglobulinemia, polychondritis, scleroderma, Wegener's
XX granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia

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CC graves, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitiligo,
 CC gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
 CC bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
 CC ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
 CC sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
 CC mellitus, uveitis, lymphopneumonia, polyarteritis nodosa, Sjogren's
 CC syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
 CC connective tissue disease, keratoconjunctivitis sicca, and vernal
 CC keratoconjunctivitis,
 XX
 SQ Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,298-99 Length: 1849
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-09-195-368-1 (1-177) x AAAT4936 (1-1849)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 DB 29 ATGTGTTGAGCCACTTGAATAATATGCTTAAGCATTCAAGACTCAAGAGACTGAG 88
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 89 AGATCATCTCGAAGCTGAGCTCTTTGCTCAATGATTATGCTATTCTTGCTCC 148
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
 DB 149 TTCAGTTGGCTATCTTTATTTTCTCCAAATTAGAGACTGCTAAGAGCCCTGATGCT 208
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 DB 209 AAGTTTGACCATTAACCTCAAAATGCAATGCAATCTTCTGAACCTCTTGCTGAAAT 268
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
 DB 269 AAGGTGCTGACTGGAAGCTGGAAGTACTTCAGATGCTTATTTATTTATGCGCAA 328
 QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGluValArgLeuTyrTrpAsn 120
 DB 329 GTGGCTCCCAATGCAATCAATGATGATGATGCTCTTTGAGGTGCGGCTGATATAAAC 388
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyTyrThrTyr 140
 DB 389 AAAGCATGATCAAACTCTTAACAAACAAATCTAAATCCAAATGTAGAGAGACTTAT 448
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 DB 449 GAATGCAATGTTGGGACCAATAGACTGATATTCACCTGCAACATCAGGCTTTTAAAA 508
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 509 AATTAACCTACTGCGGTATCATTTTACTAGCAAAATCCCAATTCATCTCC 559
 RESULT 6
 AA257314 standard; cDNA; 1849 BP.
 ID AA257314;
 AC AA257314;
 XX
 XX 03-APR-2000 (first entry)
 DE Human endokine alpha protein encoding cDNA SEQ ID NO:1.
 XX
 XX Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
 KM immunomodulation; inflammation; cell proliferation; angiogenesis;
 KW tumour metastasis; apoptosis; sepsis; endotoxemia; ds.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT CDS 53..562
 FT /tag= a
 FT /product= "endokine alpha"
 XX
 XX US5998171-A.
 XX PD 07-DEC-1999.
 XX
 XX
 XX 15-AUG-1997; 97US-00912227.
 XX
 XX 16-AUG-1996; 96US-0024058P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Ni J, Rosen CA, Yu G,
 DR WPI; 2000-104608/09.
 DR P-PSDB; AAY53061.
 XX
 XX Isolated human endokine alpha gene useful as a diagnostic probes and
 PT primers.
 XX
 XX Claim 3; Fig 1; 31pp; English.
 XX
 CC The present sequence encodes human endokine alpha which is a member of
 CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha
 CC protein and polynucleotides can be used in diagnostic and therapeutic
 CC methods concerning TNF family-related disorders. These include disorders
 CC associated with immunomodulation and inflammation, cell proliferation,
 CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxemia
 XX
 SQ Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,298-99 Length: 1849
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-09-195-368-1 (1-177) x AA257314 (1-1849)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 DB 29 ATGTGTTGAGCCACTTGAATAATATGCTTAAGCATTCAAGACTCAAGAGACTGAG 88
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 89 AGATCATCTCGAAGCTGAGCTCTTTGCTCAATGATTATGCTATTCTTGCTCC 148
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaLysGluProCysMetAla 60
 DB 149 TTCAGTTGGCTATCTTTATTTTCTCCAAATTAGAGACTGCTAAGAGCCCTGATGCT 208
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 DB 209 AAGTTTGACCATTAACCTCAAAATGCAATGCAATCTTCTGAACCTCTTGCTGAAAT 268
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
 DB 269 AAGGTGCTGACTGGAAGCTGGAAGTACTTCAGATGCTTATTTATTTATGCGCAA 328
 QY 329 GTGGCTCCCAATGCAATCAATGATGATGATGCTCTTTGAGGTGCGGCTGATATAAAC 388
 QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGluValArgLeuTyrTrpAsn 120
 DB 449 GAATGCAATGTTGGGACCAATAGACTGATATTCACCTGCAACATCAGGCTTTTAAAA 508
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyTyrThrTyr 140
 DB 389 AAAGCATGATCAAACTCTTAACAAACAAATCTAAATCCAAATGTAGAGAGACTTAT 448

QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlyValLeuLys 160
 DB 449 GAATGGACATGTTGGGACACCAACAGCTGATATTCACCTGACATGAGCTTCAAAA 508
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 509 AATATATCTACTGGGGTATCATTTTACTATGCAAAATCCCAATTATCTCC 559
 RESULT 7
 ADAL1463
 ID ADAL1463 standard; cDNA, 1849 BP.
 XX
 AC ADAL1463;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human endokine alpha cDNA.
 XX
 KW human; endokine alpha; melanoma; sarcoma; tumour; tumour regression;
 KW infection; viral; bacterial; yeast; fungal; Toxoplasma gondii;
 KW Schistosoma mansoni; Listeria monocytogenes; tumour necrosis factor;
 KW TNF-related disorder; endokine alpha-related disorder; immunomodulation;
 KW inflammation; cell proliferation; angiogenesis; tumour metastasis;
 KW apoptosis; sepsis; endotoxaemia; ss; gene.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 53..562
 FT /tag=a
 FT /product="Endokine alpha"
 FT
 FN US2002099198-A1.
 XX 25-JUL-2002.
 XX
 PF 01-JUL-1999; 99US-00345790.
 XX
 XX 16-AUG-1996; 96US-0024058P.
 PR 15-AUG-1997; 97US-00912227.
 XX
 PA (YUGG/) YU G.
 PA (NIJ/) NI J.
 PA (ROSE/) ROSEN C A.
 XX
 PT Yu G, Ni J, Rosen CA;
 DR P-PSDB; ADA11464.
 XX
 PT Novel isolated endokine alpha polypeptide, a member of tumor necrosis
 PT factor ligand family, and antibodies against the polypeptides, useful for
 PT treating melanoma, sarcoma, and viral, bacterial, fungal infections.
 XX
 PS Claim 5; Fig 1; 29pp; English.
 XX
 CC The invention relates to an isolated human endokine alpha polypeptide. A
 CC cell recombinant for the human endokine alpha polypeptide is useful for
 CC producing the protein by recombinant techniques. The antigenic epitope
 CC bearing peptides and polypeptides are useful to raise antibodies
 CC including monoclonal antibodies. The peptides and antibody antibodies
 CC are used in a variety of qualitative or quantitative assays for the
 CC protein. The protein is useful for tumour targeting and thus used in
 CC patients with melanoma and sarcoma for tumour regression and extension of
 CC patient life-span through a local injection. the protein is also useful
 CC for treating viral, bacterial, yeast, fungal and other infections e.g.,
 CC Toxoplasma gondii, Schistosoma mansoni, Listeria monocytogenes etc. The
 CC protein is also useful for treating other tumour necrosis factor (TNF)-
 CC related disorders. The nucleic acid is useful as probes for gene mapping
 CC by in situ hybridisation and for detecting expression of endokine alpha
 CC gene in human tissue e.g. by Northern blot analysis. The nucleic acid is
 CC also useful for diagnosing an endokine alpha-related disorder such as
 CC disorders associated with immunomodulation and inflammation, cell

CC proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or
 CC endotoxaemia. The antibody is useful diagnostically or therapeutically as
 CC antagonists in the treatment of alpha and/or TNF-related disorders. The
 CC antibody is also useful for purification of the protein. The antibodies
 CC are useful for detecting the protein and for tracking the fate of various
 CC regions of a protein precursor which undergoes post-translational
 CC processing. The present sequence represents cDNA encoding human endokine
 CC alpha.
 XX
 SQ Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,29e-99 Length: 1849
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-09-195-368-1 (1-177) x ADAL1463 (1-1849)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 DB 29 ATGTTTGAGCCCACTGGAAAAATATGCTTTTAAAGCATTCAGAACTCAAGAGAGCTCAG 88
 QY ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 89 AGATCATCTCGAAGAGCTGCTGCTTTTGTCTCAATGTTATGTTGCTTCTTGTCTCC 148
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGluProCysMetAla 60
 DB 149 TTCAGTTGGCTAACTTTATTTCTTCCAAATTAGAGCTCTTAGAGGCCCTGTATGGCT 208
 QY 61 LysPheGlyProLeuProSerLysTrpGluMetAlaSerSerGluProProCysValAsn 80
 DB 209 AAGTTTGAGCATTAACCTCAAAATGSCAAATGSCAATCTTGAACCTCTTCCGCTGAAT 268
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGlyGln 100
 DB 269 AAGGTGTCTGCTGAGAGCTGAGATGATCTTCAAGATGCTTATTTATTTATGGCCAA 328
 QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGluValArgLeuTyrLysAsn 120
 DB 329 GTGGCTCCCAATGCAATCTCAATGATGATGCTCTTCTTATGAGTGCGGCTGTATAAAAAC 388
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyIleTyr 140
 DB 389 AAAGACATGATPACAACTTACCAACCAATCTTAAATCCAAATGTAAGAGGAGACTTAT 448
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlyValLeuLys 160
 DB 449 GAATGGACATGTTGGGACACCAACAGCTGATATTCACCTGACATGAGCTTCAAAA 508
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 509 AATATATCTACTGGGGTATCATTTTACTATGCAAAATCCCAATTATCTCC 559
 RESULT 8
 ADC01857
 ID ADC01857 standard; cDNA, 1849 BP.
 XX
 AC ADC01857;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human cDNA encoding Endokine alpha.
 XX
 KW Human; ss; gene; endokine alpha; tumour necrosis factor family; AIDS;
 KW chronic lymphocyte disorder; tumour; parasitic disease;
 KW autoimmune disease; lupus; arthritis; multiple sclerosis; inflammation;
 KW graft versus host disease; transplant rejection; skin allergy;
 KW bowel disease; wound; sepsis; Hodgkin's disease;
 KW chronic lymphocyte leukaemia; Burkitt's lymphoma; scleroderma;

chronic active hepatitis; myasthenia gravis; psoriasis;
 autoimmune thyroiditis; Goodpasture's disease; asthma; Graves disease;
 cirrhosis; insulin dependent diabetes mellitus; Sjogren's syndrome;
 glomerulonephritis; hepatitis; Parkinson's disease; atherosclerosis;
 rheumatoid arthritis.
 Homo sapiens.
 Location/Qualifiers
 Key 53..562
 FT /*tag= a
 FT /product= "Endokine alpha"
 US2002168729-A1.
 14-NOV-2002.
 02-MAY-2002; 2002US-00136511.
 16-AUG-1996; 96US-0024058P.
 15-AUG-1997; 97US-00912227.
 26-FEB-1999; 99US-0122099P.
 28-MAY-1999; 99US-0136788P.
 01-JUL-1999; 99US-00345790.
 25-FEB-2000; 2000US-00513584.
 (HUMA-) HUMAN GENOME SCI INC.
 Yu G, Ni J, Rosen CA;
 WPI; 2003-755026/71.
 Novel isolated endokine alpha polypeptide AIDS, chronic lymphocyte
 disorder, common variable immunodeficiency, a tumor, parasitic disease,
 autoimmune disease, lupus, arthritis, multiple sclerosis.
 Claim 1; SEQ ID NO 1; 90pp: English.
 The invention relates to an isolated endokine alpha polypeptide (a member
 of the tumor necrosis factor family), appearing as ADC01857, the
 sequence of the endokine alpha polypeptide having an sequence encoded by
 the cDNA clone contained in ATCC Deposit number 97640 (A1) and the
 sequence of an epitope-bearing portion of the above polypeptides. Also
 included are the encoding nucleic acid (its homologues, complements or
 fragments where the fragment comprises at least 50 contiguous
 nucleotides), provided that the fragment is not from a region starting at
 nucleotide 26 and ending at nucleotide 476 of ADC01857, making a
 recombinant vector comprising the nucleic acid and an isolated antibody
 or antibody fragment that binds specifically to endokine alpha. The DNA
 and protein are useful for treating an individual having a disorder
 chosen from AIDS, chronic lymphocyte disorder, common variable
 immunodeficiency, a tumor, parasitic disease, autoimmune disease, lupus,
 arthritis, idiopathic thrombocytopenic purpura, multiple sclerosis,
 chronic inflammation, acute inflammation, acute allograft rejection,
 graft versus host disease, transplant rejection, foetal resorption,
 fecal peritonitis, skin allergies, bowel disease, a wound, sepsis, ALL,
 Hodgkin's disease, non-Hodgkin's lymphoma, chronic lymphocyte leukaemia,
 plasmacytomas, multiple myeloma, Burkitt's lymphoma, EBV-transformed
 disease, chronic myelogenous leukaemia, chronic hyperimmunoglobulinemia,
 autoimmune haematological disorders, polychondritis, scleroderma, Wegener
 granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
 gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, autoimmune
 thyroiditis, idiopathic Addison's disease, vitiligo, gluten-sensitive
 enteropathy, autoimmune neutropenia, pemphigus vulgaris, Goodpasture's
 disease, bullous pemphigoid, discoid lupus, dense deposit disease,
 endocrine ophthalmopathy, IBD, asthma, Graves disease, sarcoidosis,
 cirrhosis, juvenile diabetes, insulin dependent diabetes mellitus,
 uveitis, autoimmune gastritis, lymphopneumonia, olivaryitis nodosa,
 Sjogren's syndrome, Bechet's disease, Hashimoto's disease, primary
 myxedema, polymyositis, mixed connective tissue disease,
 keratoconjunctivitis sicca, vernal keratoconjunctivitis, interstitial
 lung fibrosis, glomerulonephritis, hepatitis, autoimmune haemolytic
 anaemia, contact sensitivity disease, Parkinson's disease, primary

lateral sclerosis, siliocosis, sarcoidosis, idiopathic pulmonary fibrosis,
 idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis,
 histamine-mediated allergic reactions, 19S-mediated allergic reactions,
 rheumatoid arthritis, plastic anaemia and myelodysplastic syndrome. The
 present sequence encodes Endokine alpha.
 Sequence 1849 BP; 562 A; 361 C; 360 G; 566 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,29e-99 Length: 1849
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0
 US-09-195-368-1 (1-177) x ADC01857 (1-1849)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 Db 29 AAGTGTGGAGCCACTTGGAAAATATGCTTTAAGCCATTCAAGAACTCAAGAGGCTCAG 88
 QY 21 ArgSerSerTrpHisLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 Db 89 AAGATCATCTCGAAGACCTGGCTCTTTGCTCAATAGTAAGTGTGCTATTTCTTGCTCC 148
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluTrpAlaIleValGluProCysMetAla 60
 Db 149 TTCAGTTGGCTAATCTTTATTTTCTCCATTAGAGATGCTAAGAGCCCTGATAGCT 208
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 209 AAGTTTGACCATTAACCTCAAAATGGCAATGGCATCTTTGAAACCTCTTGCTGAT 268
 QY 81 LysValSerAspTrpLeuLeuGluIleLeuGlnAsnGlyLeuTrpLeuIleTyrGlyGln 100
 Db 269 AAGGTCTCTGACTGGAAGCTGGAAGTCTTCAAGATGCTTATTTATTTATTTATGCGCA 328
 QY 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGluValArgLeuTrpLysAsn 120
 Db 329 GGGCTCCCAATGACCAATCAATGATGATGCTTTGAGGCGGCTGTATTAATAAAC 388
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleValGlnAsnValGlyTyr 140
 Db 389 AARGCATGATACCAACTCTAACCAACCAATCTAAATCCAAATGTAGGAGGACTTAT 448
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 449 GAATTCATGTTGGGGAACCATAGACTGATATTTCAACTGTGAGCATCAGTTCTTAAA 508
 QY 161 AsnAsnTrpTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 509 AATATACCTACTGGGGGATCATTTTACTACCAATCCCAATTCATCTCC 559
 RESULT 9
 ID AAX59844 standard; CDNA. 1964 BP.
 AAX59844;
 28-JUL-1999 (first entry)
 CDNA sequence for human DNA19355.
 DNA19355; tumour necrosis factor homologue; receptor GTR; immunogen;
 antibody; apoptosis; mammalian cancer cell;
 tumour necrosis factor (TNF)-alpha secretion; primary T-cell;
 proinflammatory response; ds.
 Homo sapiens.
 MO9925834-A1.

PD 27-MAY-1999.
 XX 18-NOV-1998; 98WO-US024621.
 PF 18-NOV-1997; 97US-0065635P.
 XX 12-DEC-1997; 97US-0069661P.
 PR (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Gurney AL, Marsters SA, Pletti R, Baker KP;
 XX Godowski PJ, Mark MR;
 PI WPI; 1999-338009/28.
 DR P-PSDB; AAY15817.
 XX New DNA19355 polypeptide as tumour necrosis factor homolog.
 XX Example 1; Fig 1; 86pp; English.
 XX The present sequence encodes a polypeptide designated DNA19355. The
 CC polypeptide is a tumour necrosis factor homologue. The DNA19355
 CC polynucleotide sequence can be used to derive hybridisation probes for
 CC e.g. isolating similar sequences, gene mapping, genetic analysis, etc.
 CC Nucleic acids which encode DNA19355 can also be used to generate
 CC transgenic or knockout animals, which are useful in the development and
 CC screening of therapeutically useful reagents. The DNA19355 polypeptides
 CC may be used in diagnostic assays to detect the presence of the receptor
 CC GTR in mammalian tissues. The polypeptides can also be used as
 CC immunogens to raise antibodies. The polypeptides may also be used to
 CC induce apoptosis in mammalian cancer cells. DNA19355 polypeptides
 CC stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-
 CC cells, and so can be used to stimulate a proinflammatory response in
 CC mammalian cells
 XX
 SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 1.4e-99 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-09-195-368-1 (1-177) x AAY59844 (1-1964)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThnGlnGlyAlaGln 20
 DB 21 ATGCTTTGAGGCACTTGGAATAATATGCTTTAGCCATTCAAGACTCAAGAGCTCAG 80
 QY 21 ArgSerSerTrpIlyLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 81 AGATCATCTCGAGAGCTGTGCTCTTTGCTCAATAGTAAATGTTGCTAATTTCTTGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThralAlaValGluProCysMetAla 60
 DB 141 TTCAGTGGCTAAATTTATTTTCTCCAAATTAAGACTGTAAGAGCCCTGATGCT 200
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 DB 201 AAGTTTGACCACTTAACCTCAAAATGCAATGCAATCTTCTGAACCTCTTGCTGAAT 260
 QY 81 LysValSerAspTrpIlyLeuGluIleLeuGlnAsnGlyLeuTrpLeuIleTrpGlyGln 100
 DB 261 AAGGCTGTGACTGAGAGCTGGAAGTACTCAAGATGCTTAATTTATTTATGCGCAA 320
 QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGluValArgLeuTrpLysAsn 120
 DB 321 GTGGCTCCCAATGCAATCAATGATGATGCTCTTTGAGTGGCGCTGTATPAAAC 380
 QY 121 LysAspMetIleGlnThleuThrasnLysSerLysIleGlnAsnValGlyGlyThTrp 140
 DB 381 AAAGCATGATACCAACTCTTAACAAACAAATCTAAATCCAAATGTAGAGGAGCTTAT 440

QY 141 GlnLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGlnHisGlnValLeuLys 160
 DB 441 GAATTCATGTTGGGGACACCATAGACTGATATTCACACTGACATCAAGGTTCTAAA 500
 QY 161 AsnAspThrTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 501 AATTAATCACTACTGGGGATTCATTTACTAGCAAAATCCCAATTCATCTCC 551
 RESULT 10
 AAX87726
 ID AAX87726 standard; cDNA; 1964 BP.
 XX AAX87726;
 AC 26-OCT-1999 (first entry)
 XX Human PRO364 ligand cDNA clone DNA19355-1150.
 DE PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;
 KM inflammation; antiinflammatory; NF-KB activation; autoimmune disease;
 KM therapy; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH CDS 21..554
 FT /*tag= a
 XX MO940196-A1.
 XX 12-AUG-1999.
 XX 09-FEB-1999; 99WO-US002642.
 PF 09-FEB-1998; 98US-0074087P.
 PR (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Gurney AL, Marsters SA, Pletti RM, Wood WI;
 PI Goddard A;
 XX WPI; 1999-494296/41.
 DR P-PSDB; AAY06646.
 DR Tumor necrosis factor receptor homologue - useful for, e.g. modulating
 PT apoptosis and NF-KB activation and proinflammatory or autoimmune
 PT responses.
 PS Example 2; Fig 5A-B; 104pp; English.
 XX This is the nucleotide sequence of a novel cDNA clone, termed DNA19355-
 CC 1150 (ATCC 209466), coding for a potential ligand (see AAY06646) of
 CC PRO364 (see AAY06605), a novel member of the tumour necrosis factor
 CC receptor family. The clone was isolated from a human umbilical vein
 CC endothelial cell cDNA library constructed in yeast transformants. PRO364
 CC polypeptides are useful for modulating apoptosis, NF-KB activation and
 CC proinflammatory or autoimmune responses in mammalian cells (claimed)
 XX
 SQ Sequence 1964 BP; 596 A; 370 C; 380 G; 616 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 1.4e-99 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-09-195-368-1 (1-177) x AAX87726 (1-1964)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThnGlnGlyAlaGln 20

Db 21 ATGTGTTGAGCCACTGGAAAAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 80
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 Db 81 AGATCATCTGTGAAGCTGTGCTCTTTTGTCCAAATGATGATGTTGATTTCTTGTCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnIleValAlaValGluProCysMetAla 60
 Db 141 TTCAGTTGGCTAATCTTTATTTTCTCCAAATTAAGATGCTGAAGAGCCCTGTATGGCT 200
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 201 AAGTTTGACCATTCCTCCAAATGCGAAATGGGATTTCTGAACCTCCTTGCGTGAAT 260
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuIleTyrglyGln 100
 Db 261 AAGGTGCTGACTGGAAGCTGGAGATACCTCAGATGCTTATTTAATTATGAGCCAA 320
 QY 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGlyValArgLeuTyrglyAsn 120
 Db 321 GTGGCTCCCAATGCAACTCAATGATGATGCTCTTTGAGGTGGCGCTGTATTAAGAAC 380
 QY 121 LysAspMetIleGlnTrpLeuThrAsnLysSerIleGlnAsnValGlyTygTrp 140
 Db 381 AAAGCATGATCAAACTCTAACAACAATCTAATAATCCAAATGTGAGAGGAGACTTAT 440
 QY 141 GluLeuHisValGlyAspTrpIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 441 GAATTGCAATGTTGGGACCACTTACATGATGATTAATCACTGAGCATCAGGTTCTAATA 500
 QY 161 AsnAsnTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 501 AATATATCACTACTGGGGTATCATTTTACTAGCAATCCCAATTCATCTCC 551

RESULT 11

AAC85435 AAC85435 standard; cDNA; 1964 BP.

AAC85435;

08-MAY-2001 (first entry)

C10me PRO175-1150.

PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;
 hGTR; ligand; hGTR; PRO175; tumor necrosis factor receptor; TNFR;
 human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;
 myocardial infarction; PGF-2alpha; trauma; cancer; angiogenesis;
 age-related macular degeneration; antibody; periodontal disease;
 vascular-related drug targeting; atherosclerosis; hypertension;
 inflammatory vasculitides; Reynaud's disease; aneurysm;
 arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
 fibrosis; neuropathy; rheumatoid arthritis; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 21..554

/tag= a

/product= "PRO175"

WO200103720-A2.

11-JUL-2000; 2000WO-US018867.

12-JUL-1999; 99US-0143304P.

(GETH) GENENTECH INC.

Williams PM, Gerritsen ME;

DR MPI, 2001-138257/14.
 DR P-PSDB; AAB47056.
 XX Composition for diagnosing and treating cardiovascular, endothelial and
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
 XX
 PS Example 2; Fig 5; 76pp; English.

CC This sequence encodes a PRO175 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor ligand (hGTR). The
 CC corresponding receptor (hGTR), PRO364, is given in AAB47054. PRO364 and
 CC PRO175 may be used in a mixture with a cardiovascular, endothelial,
 CC angiogenic or angiostatic agent for the treatment of a cardiovascular,
 CC endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was
 CC isolated from an expressed sequence tag (EST) database as having homology
 CC to members of the tumor necrosis factor receptor (TNFR) family of
 CC polypeptides. The PRO175 cDNA sequence was isolated from a library of
 CC cDNA fragments derived from human umbilical vein endothelial cells
 CC (HUVEC). Administering an effective amount of PRO364 or PRO175 or their
 CC antagonists is useful for treating cardiac hypertrophy (which is
 CC initiated by myocardial infarction and characterized by the presence of
 CC an elevated level of PGF-2alpha), trauma, a cancer, or age-related
 CC muscular degeneration in a human. Administering a therapeutically
 CC effective amount of an antibody that binds PRO364 or PRO175 is useful for
 CC inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering
 CC from a tumor or a retinal disorder. PRO364 or PRO175, or their
 CC antagonists, are useful for vascular-related drug targeting or as
 CC therapeutic targets for the treatment or prevention of atherosclerosis,
 CC hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,
 CC arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection
 CC or regeneration and treatment of lung or liver fibrosis, periodontal
 CC diseases, attraction of bone-forming cells, central and peripheral
 CC nervous system disease and neuropathies and rheumatoid arthritis
 XX

SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.: 1..4e-99 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-195-368-1 (1-177) x AAC85435 (1-1964)

QY 1 MetCysLeuSerHisLeuGlnAsnMetProLeuSerHisSerArgThrGlnIleValGln 20
 Db 21 ATGTGTTGAGCCACTGGAAAAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 80
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 Db 81 AGATCATCTGTGAAGCTGTGCTCTTTTGTCCAAATGATGATGTTGATTTCTTGTCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnIleValAlaValGluProCysMetAla 60
 Db 141 TTCAGTTGGCTAATCTTTATTTTCTCCAAATTAAGATGCTGAAGAGCCCTGTATGGCT 200
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 201 AAGTTTGACCATTCCTCCAAATGCGAAATGGGATTTCTGAACCTCCTTGCGTGAAT 260
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuIleTyrglyGln 100
 Db 261 AAGGTGCTGACTGGAAGCTGGAGATACCTCAGATGCTTATTTAATTATGAGCCAA 320
 QY 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGlyValArgLeuTyrglyAsn 120
 Db 321 GTGGCTCCCAATGCAACTCAATGATGATGCTCTTTGAGGTGGCGCTGTATTAAGAAC 380
 QY 121 LysAspMetIleGlnTrpLeuThrAsnLysSerIleGlnAsnValGlyTygTrp 140
 Db 381 AAAGCATGATCAAACTCTAACAACAATCTAATAATCCAAATGTGAGAGGAGACTTAT 440

QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 CC 141 GAAATGGCATGTTGGGGACACCATAGACTTGATATTCACACTGAGCATCGAGTCTTCAAA 500
 Db 441 GAAATGGCATGTTGGGGACACCATAGACTTGATATTCACACTGAGCATCGAGTCTTCAAA 500
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 CC 161 AATAATACATCTGGGGATCATTTTACTAGCAAAATCCCAATTCATCTCC 551
 Db 501 AATAATACATCTGGGGATCATTTTACTAGCAAAATCCCAATTCATCTCC 551
 RESULT 12
 AAF30051
 ID AAF30051 standard; cDNA; 1964 BP.
 XX AAF30051;
 AC AAF30051;
 XX 30-APR-2001 (first entry)
 DT 30-APR-2001 (first entry)
 XX Human cDNA encoding PRO175.
 DE PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;
 KW antiarthritic; antiinflammatory; antianemic; immunosuppressive;
 KW antidiabetic; neuroprotective; hepatocytic; virucide;
 KW dermatological; antipsoriatic; antiallergic; antiallergic;
 KW immunostimulant; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 PH CDS 21..554
 FT sig_peptide 21..152
 FT /*tag= b
 FT mat_peptide 153..551
 FT /*tag= c
 XX MO200105972-A1.
 XX 25-JAN-2001.
 XX 15-MAR-2000; 2000MO-US006884.
 XX 20-JUL-1999; 99US-0144758P.
 XX (GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ,
 PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
 PI Watanabe CK, Wood WI;
 XX WPI, 2001-103149/11.
 DR P-PSDB; AAB20109.
 DR New PRO polypeptides, nucleic acids and (ant)agonists, useful for
 PT diagnosing and treating immune-related disorders, such as multiple
 PT sclerosis, rheumatoid arthritis and diabetes.
 XX Claim 21; Fig 3; 127bp; English.
 XX The present sequence is that of cDNA clone DNA19355-1150 (ATCC 209466)
 CC encoding novel human immunomodulator protein PRO175 (UNQ149) (see
 CC AAB20109). The clone was isolated from a yeast screening of human cDNA.
 CC The predicted protein (20 kDa, pI 8.08) shows homology to members of the
 CC tumour necrosis factor family. The invention provides polynucleotides
 CC (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)
 CC including PRO175. Claimed compositions comprising these proteins or their
 CC agonists are useful for increasing infiltration of inflammatory cells
 CC into a tissue of a mammal, stimulating or enhancing an immune response in
 CC a mammal, or increasing the proliferation of T-lymphocytes in a mammal in
 CC response to an antigen. Claimed compositions comprising the PRO
 CC polypeptide or its antagonist have the opposite effect. A claimed method
 CC for treating an immune related disorder, such as a T cell disorder,
 CC involves administering the PRO polypeptide, an agonist antibody or an
 CC antagonist antibody. The disorder is selected from systemic lupus

CC erythematous, rheumatoid arthritis, osteoarthritis, juvenile chronic
 CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia,
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,
 CC demyelinated diseases (such as multiple sclerosis), autoimmune chronic
 CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,
 CC sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis
 CC and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,
 CC (auto)immune-mediated skin diseases (such as bullous skin disease,
 CC erythema multiforme and psoriasis), allergic diseases (such as asthma,
 CC allergic rhinitis, atopic dermatitis, food hypersensitivity and
 CC urticaria), immunologic diseases of the lung and transplantation
 CC associated diseases (such as graft rejection and graft-versus-host
 CC disease) (all claimed). Claimed methods of diagnosing these disorders
 CC comprise detecting the level of expression of the PRO gene. Also claimed
 CC are a method of identifying a compound capable of inhibiting the
 CC expression or activity of the PRO polypeptide, vectors, host cells,
 CC antibodies, and a method of stimulating an immune response in a mammal
 CC using PRO175
 CC
 XX SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 1,4e-99 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: Gaps: 0
 US-09-195-368-1 (1-177) x AAF30051 (1-1964)
 QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 Db 21 ATGTGTTTGAGCCACTGGAAAATATGCTTTACGCCATTCACAGACTCAAGAGACTCAG 80
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 Db 81 AGATCATCTCGAAGCTGAGCTGCTTTGCTCAATAGTAAGTATGTTCTTCTTGGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnIleValAlaValGlnProCysMetLeu 60
 Db 141 TTCAGTTGGCTAATCTTATTTTCTCCAAATTAGAGACTGCTCAAGAGACTCGTAGGCT 200
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 201 AGCTTGAACCATACCCCAAAATGCAATGGCATCTTCGAACCTCTTGCGCTGAT 260
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGln 100
 Db 261 AAGGTGCTCGACTGAGAGCTGAGAGTACTCGAATGCTTATTTATTTATTTATGCGCA 320
 QY 101 ValAlaProAsnAlaAsnTyrAspValAlaProPheGlnValArgLeuTyrLysAsn 120
 Db 321 GTGGCTCCCAATGCAACTACATCATGTAGCTCTTTTGAGTGGCTGCTATTAATC 380
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyLeuTyr 140
 Db 381 AAGGACATATACAAACTTAACAACAATCTAAATCCAAATGTTGAGGAGGACTAT 440
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 441 GAAATGGCATGTTGGGGACACCATAGACTTGATATTCACACTGAGCATCGAGTCTTCAAA 500
 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 501 AATAATACATCTGGGGATCATTTTACTAGCAAAATCCCAATTCATCTCC 551
 RESULT 13
 AAC97374
 ID AAC97374 standard; cDNA; 1964 BP.
 XX

AC AAC97374;
 XX 28-FEB-2001 (first entry)
 XX
 DE Human angiogenesis-associated protein PRO175 cDNA, SEQ ID NO:8.
 XX
 XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;
 KW gene therapy; transgenic animal; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200053753-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 05-JAN-2000; 2000W0-US000219.
 XX
 PR 08-MAR-1999; 99W0-US0050228.
 PR 12-MAR-1999; 99US-0123957P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1998; 99W0-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99W0-US020111.
 PR 08-SEP-1999; 99W0-US020594.
 PR 15-SEP-1999; 99W0-US021090.
 PR 15-SEP-1999; 99W0-US021547.
 PR 05-OCT-1999; 99W0-US023089.
 PR 30-NOV-1999; 99W0-US028313.
 PR 30-NOV-1999; 99W0-US028409.
 PR 02-DEC-1999; 99W0-US028564.
 PR 02-DEC-1999; 99W0-US028565.
 XX
 PA (GENTECH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
 PI Gadoweki PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
 PI Paoni NF, Pletti RM, Watanabe CK, Williams PM, Wood WI;
 XX
 DR WPI; 2001-090793/10.
 XX P-PSDB; AAB53065.
 XX
 PT New isolated nucleic acid for producing a PRO polypeptide, analyzing
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic
 PT disorders, such as atherosclerosis, wounds or cancer.
 XX
 PS Claim 58; Fig 3A-B; 293pp; English.
 CC The invention relates to novel human angiogenesis-associated proteins
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding
 CC PRO proteins. The invention also relates to vectors and host cells
 CC comprising a PRO nucleic acid, the recombinant production of a PRO
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and
 CC compounds which inhibit the expression of a PRO gene. The invention
 CC additionally encompasses methods of identifying modulators of PRO
 CC expression or activity; diagnosing a cardiovascular, endothelial or
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting
 CC mutations in a PRO gene, or the expression level of a PRO gene within a
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO
 CC agonists and PRO antagonists may be used as therapeutic agents to treat

CC cardiovascular, endothelial or angiogenic disorders, such as
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's
 CC disease, or stroke. PRO nucleic acids are additionally useful in the
 CC recombinant production of PRO proteins, as hybridisation probes to screen
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals
 CC useful for the development and screening of potential therapeutic agents.
 CC The present sequence represents a cDNA encoding a PRO protein of the
 CC invention
 XX
 SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,4e-99 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 DB 81 AGATCATCCTGAGAACCTGGCTCTTTGCTCAAAAGTAGTAGTTGCTATTTCTTTGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnIleValaValaValaProCysMetAla 60
 DB 141 TTCAGTGGCTAATCTTTATTTTCTTCCAAATAGAGACTGCTAAAGAGACCCGTATGGCT 200
 QY 61 LysPheGlyProLeuProSerSerLysTrpGlnMetAlaSerSerGlnProProCysValaAsn 80
 DB 201 AAGTTTGACCATTTACCCCTCAAAATGGCAAAATGGGAGATCTTCTGAAACCTTCGCGTGAAT 260
 QY 81 LysValSerAspTrpLysLeuGluIleLeuGlnaGlnValaValaValaValaValaVala 100
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 DB 321 GTGGCTCCCAATGCAAACTAACAATGATGATGCTCTTTGAGGTGCGCTGTAATAAAC 380
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValaValaValaVala 140
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 QY 141 GluLeuHisValaGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValaLeuLys 160
 DB 441 GAATTCATGTTGGGAGACCAATACCTGATATTCATCTGAGCATCAGGATCTCAAAA 500
 QY 161 AsnAsnThrTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheLeuSer 177
 DB 501 AATTAATACACTACGGGGTATCAATTTACTAGCAAAATCCCAATATCATCTCC 551
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 AAC85945
 ID AAC85945 standard; cDNA; 1964 BP.
 XX
 AC AAC85945;
 AC
 XX 22-AUG-2001 (first entry)
 DT
 XX Native sequence of PRO175 cDNA, clone DNA19355-1150-1.
 DE
 KW PRO; type II transmembrane protein; tumour necrosis factor; stroke;
 KW heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;

KW myocardial infarction; cardiac hypertrophy; Pgf 2alpha; trauma; bone;
 KW cancer; age-related macular degeneration; wound; burn; hypertension;
 KW diabetes mellitus; osteoporosis; ischemia; atherosclerosis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; amyotrophic lateral sclerosis;
 KW endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; ss.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
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 FT /product= "PRO175 polypeptide"
 FT sig_peptide 16..95
 FT /*tag= b
 FT mat_peptide 96..551
 FT /*tag= c
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 PN WO200140464-A1.
 XX
 PD 07-JUN-2001.
 XX
 PF 11-AUG-2000; 2000WO-US022031.
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 PR 30-NOV-1999; 99WO-US028313.
 XX
 PR 30-NOV-1999; 99WO-US028409.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 28-JUL-2000; 2000WO-US020710.
 XX
 PA (GENE) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Ferrara N, Godowski PJ, Gurney AJ;
 PI Hillan KJ, Mark MR, Marsters SA, Paoi NF, Pletti RM, Wood WI;
 DR WPI; 2001-381383/40.
 DR P-PEDB; AAB47287.
 XX
 PT Isolated PRO polypeptide useful in treating and diagnosing a
 PT cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes
 PT mellitus, myocardial infarction, arthritis.
 XX
 PS Claim 57; Fig 1; 144pp; English.
 XX
 CC The sequences given in AAC65945-48 encode PRO polypeptides. PRO175 shows
 CC type II transmembrane protein topology, and portions of PRO364 show
 CC homology to members of the tumour necrosis factor (TNF) family, thereby
 CC indicating that it may be a novel member of the TNF family. PRO175 and
 CC PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a
 CC compound that inhibits PRO, diagnosing a cardio-vascular, endothelial or
 CC angiogenic disorder in a mammal by detecting PRO cDNA, treating
 CC cardiovascular, endothelial or angiogenic disorder in a mammal, and
 CC inducing cardiac hypertrophy or inhibiting endothelial cell growth or
 CC angiogenesis in a mammal. The mammal is a human which has suffered
 CC myocardial infarction, cardiac hypertrophy characterized by the presence
 CC of elevated Pgf 2alpha, trauma, cancer or age-related diseases
 CC degeneration. Trauma includes wounds or burns. Other treatable diseases
 CC include diabetes mellitus, osteoporosis, ischemia, hypertension,
 CC rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,
 CC endometriosis, angina, neoplasms, periodontal disease, bone and cartilage
 CC repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,
 CC amyotrophic lateral sclerosis, and stroke
 XX
 SQ Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:
 Pred. No.: 1.4e-99 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-09-195-368-1 (1-177) x AAC65945 (1-1964)
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 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaIleGluProCysMetAla 60
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 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTrpLeuIleTrpGlyGln 100
 Db 261 AAGTGTCTGACTCGAAGCTGAGATATTCAAGAAATGGCTTATTTATTTATTTATGAGCCAA 320
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 Db 381 AAAGATGATATCAAACTTAACAATTAACAATTAACAATTAACAATTAACAATTAACAATTA 440
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 441 GAATTCATGTTGGGACCACTTAAGATCTGATTAATCACTGACACATCAGGTTCTTAAAA 500
 QY 161 AsnAsnThrTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 501 AATTAATCACTAGGCTTATTTTATTTTACAGCAATCCCAATTCATCTCC 551
 RESULT 15
 AAC90563 standard; cDNA; 1964 BP.
 XX AAC90563;
 AC
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Human PRO175 cDNA.
 XX
 KW Human; PRO; cardiac; antiangiogenic; antiarteriosclerotic; hypotensive;
 KW vasotropic; antiinflammatory; antiarthritis; antiinflammatory; cytostatic;
 KW vulnerary; antiangiinal; gene therapy; cardiovascular disease;
 KW endothelial disorder; angiogenic disorder; cancer; periodontal disease;
 KW wound healing; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073445-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013705.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 30-NOV-1999; 99WO-US028313.

30-NOV-1999; 99MO-US028409.
 PR 02-DEC-1999; 99MO-US028565.
 PR 16-DEC-1999; 99MO-US030095.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 18-FEB-2000; 2000MO-US004342.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 10-MAR-2000; 2000MO-US006319.
 PR 15-MAR-2000; 2000MO-US006884.
 PR 21-MAR-2000; 2000MO-US007532.
 PR 30-MAR-2000; 2000MO-US008439.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME,
 PI Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Masters SA,
 PI Peoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI,
 XX
 DR WPI, 2001-025251/03.
 DR P-PSDB; AAB50951.
 XX
 XX

Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal.

Claim 60; Fig 1; 182pp; English.

The present sequence is one of seventeen nucleic acids encoding PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumor angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.

Sequence 1964 BP; 596 A; 369 C; 381 G; 616 T; 0 U; 2 Other;

Alignment Scores:

Pred. No.:	Length:	1964
Score:	951.00	177
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
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DB:	4	Gaps: 0

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 QY 21 ArgSerSerTrpPheLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 Db 81 AGATCAATCCCGAAGCTGTGCTCTTGGCTCAATAGTATGTTGCTATTCTTGGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaIleGluProCysMetAla 60
 Db 141 TTCAGTGGCTATCTTATTTCTCCATTAGAGACTGCTAAGAGCCCTGTATGGCT 200
 QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
 Db 201 AAGTTGACCATTAACCTCAAAATGGCAATGGCATCTTTCGAACTCTTGGCGAAT 260
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Db 261 AAGTGTCTGACTGGAACTGGAGATACCTTCAGAAATGCTTATTTAATTATGCCCCA 320
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 QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 501 AATATACATACCTGGGCTATCATTTTACTAGCAATCCCAATTCATCTCC 551

Search completed: April 7, 2004, 17:08:46
 Job time : 332.795 secs

GenCore version 5.1.6
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Run on: April 7, 2004, 18:25:49 ; Search time 277.896 Seconds

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Database: Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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2	951	100.0	534	14	US-10-272-411-9	Sequence 9, Appl
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4	951	100.0	534	14	US-10-272-328A-9	Sequence 9, Appl
5	951	100.0	534	14	US-10-310-793-43	Sequence 43, Appl
6	951	100.0	1849	9	US-09-345-790-1	Sequence 1, Appl
7	951	100.0	1849	13	US-10-136-511-1	Sequence 1, Appl
8	951	100.0	1964	13	US-10-080-455-2	Sequence 2, Appl
9	951	100.0	1964	13	US-10-116-378-15	Sequence 15, Appl
10	951	100.0	1964	13	US-10-116-378-27	Sequence 27, Appl
11	281	29.5	162	9	US-09-864-761-32533	Sequence 32533, A
12	170	17.9	397	9	US-09-864-961-16032	Sequence 16032, A
13	107	11.3	60	10	US-09-908-975-14130	Sequence 14130, A
14	92	9.7	50	15	US-10-131-827-2732	Sequence 2732, Ap
15	88	9.3	686	15	US-10-027-632-287892	Sequence 287892, A
16	86.5	9.1	455	10	US-09-188-995-28735	Sequence 28735, A
17	86	9.0	755	15	US-10-027-632-11649	Sequence 11649, A
18	85.5	9.0	885	15	US-10-027-632-11449	Sequence 11449, A
19	85.5	9.0	3441	15	US-10-295-027-279	Sequence 279, App
20	85.5	9.0	3650	14	US-10-037-270-30	Sequence 30, Appl
21	85.5	9.0	3650	15	US-10-117-722-30	Sequence 30, Appl
22	84.5	8.9	1008	10	US-09-951-061A-130	Sequence 942, App
23	84.5	8.9	1727	9	US-09-834-975-542	Sequence 27503, A
24	84.5	8.9	2829	15	US-10-369-493-27503	Sequence 287, App
25	82.5	8.7	1767	9	US-09-832-849A-287	Sequence 75, Appl
26	82.5	8.7	8372	12	US-10-221-714A-75	Sequence 43801, A
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32	80.5	8.5	2196	15	US-10-640-252-3	Sequence 10, Appl
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37	80	8.4	17509	9	US-09-880-107-2097	Sequence 285, App
38	80	8.4	149480	10	US-09-873-367C-284	Sequence 58420, A
39	80	8.4	149480	12	US-10-873-367C-285	Sequence 2385, Ap
40	79.5	8.4	875	9	US-09-764-877-2385	Sequence 224303, A
41	79.5	8.4	16086	15	US-10-242-515-22385	Sequence 224304, A
42	79.5	8.4	611	15	US-10-027-632-224303	Sequence 13, Appl
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ALIGNMENTS

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US-10-202-062-39
Sequence 39, Application US/10202062
Publication NO. US20040038349A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PFS59
CURRENT APPLICATION NUMBER: US/10/202,062
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,838
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 39
LENGTH: 534
TYPE: DNA
ORGANISM: human
US-10-202-062-39

Alignment Scores:
Pred. No.: 3,93e-120 Length: 534
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
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US-09-195-368-1 (1-177) x US-10-202-062-39 (1-534)

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QY 21 ArgSerSerTrpIleuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 61 AGATCATCTGGAAGCTGGCTCTTTGCTCAATGATGATGCTATTTCTTGCTCC 120

QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaIysGluProCysMetAla 60
 DB 121 TTCAGTTGGCTAATCTTATTTTCTCCAAATTAGAGCTGTAAGAGCCCTGTATGCT 180

QY 61 LysPheGlyProLeuProSerIleTrpGlnMetAlaSerSerGluProProCysValAsn 80
 DB 181 AAGTTTGACCACTTGGAATAATATGCTTTAAGCATTCAGAACTCAAGAGGCTCAG 240

QY 81 LysValSerAspTrpIleuTrpLeuGluIleLeuGlnAsnGlyLeuTrpGlyGln 100
 DB 241 AAGGCTCTGAGCTGGAAGCTGGAAGTACTTCAAGATGCTTATTTAATTATAGCCAA 300

QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGluValArgLeuTrpLysAsn 120
 DB 301 GTGGCTCCCAATGCAAACTGACATGATGATGCTCTTTGAGGCGCTGTATATAAAC 360

QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValGlyGlyThrTyr 140
 DB 361 AAAGCATGATGACCACTTGGAATAATATGCTTTAAGCATTCAGAACTCAAGAGGCTCAG 420

QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 DB 421 GAATTCATGTTGGGACACCATGATGATGATGATGATGATGATGATGATGATGATGAT 480

QY 161 AsnAsnTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 481 AATAATACATCTGGGGTATCATTTTACTAGCAATCCCAATTCATCTCC 531

RESULT 2
 US-10-272-411-9
 ; Sequence 9, Application US/10272411
 ; Publication No. US20030100068A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Barnes Jewish Hospital
 ; APPLICANT: Lam, Jonathan
 ; APPLICANT: Rose, F. Patrick
 ; APPLICANT: Teitelbaum, Steven
 ; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
 ; FILE REFERENCE: 60019620-0202
 ; CURRENT APPLICATION NUMBER: US/10/272,411
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: 60/329,393
 ; PRIOR FILING DATE: 2001-10-15
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 534
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: NCBI/NM_005092.1
 ; DATABASE ENTRY DATE: 2002-10-07
 ; RELEVANT RESIDUES: (1)..(534)
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: NCBI/AF125303.1
 ; DATABASE ENTRY DATE: 1999-07-02
 ; RELEVANT RESIDUES: (1)..(534)
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: NCBI/AF117713.1

DATABASE ENTRY DATE: 1999-08-09
 RELEVANT RESIDUES: (1)..(534)
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: NCBI/AL031599.1
 DATABASE ENTRY DATE: 1999-11-23
 RELEVANT RESIDUES: (1)..(534)
 US-10-272-411-9

Alignment Scores:
 Pred. No.: 3,936-120 Length: 534
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14 Gaps: 0

US-09-195-368-1 (1-177) x US-10-272-411-9 (1-534)

QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 DB 1 ATGTGTTGACCACTTGGAATAATATGCTTTAAGCATTCAGAACTCAAGAGGCTCAG 60

QY 21 ArgSerSerTrpIleuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
 DB 61 AGATCATCTGGAAGCTGGCTCTTTGCTCAATGATGATGCTATTTCTTGCTCC 120

QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaIysGluProCysMetAla 60
 DB 121 TTCAGTTGGCTAATCTTATTTTCTCCAAATTAGAGCTGTAAGAGCCCTGTATGCT 180

QY 61 LysPheGlyProLeuProSerIleTrpGlnMetAlaSerSerGluProProCysValAsn 80
 DB 181 AAGTTTGACCACTTGGAATAATATGCTTTAAGCATTCAGAACTCAAGAGGCTCAG 240

QY 81 LysValSerAspTrpIleuTrpLeuGluIleLeuGlnAsnGlyLeuTrpGlyGln 100
 DB 241 AAGGCTCTGAGCTGGAAGCTGGAAGTACTTCAAGATGCTTATTTAATTATAGCCAA 300

QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGluValArgLeuTrpLysAsn 120
 DB 301 GTGGCTCCCAATGCAAACTGACATGATGATGATGATGATGATGATGATGATGATGAT 360

QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerIleGlnAsnValGlyGlyThrTyr 140
 DB 361 AAAGCATGATGACCACTTGGAATAATATGCTTTAAGCATTCAGAACTCAAGAGGCTCAG 420

QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 DB 421 GAATTCATGTTGGGACACCATGATGATGATGATGATGATGATGATGATGATGATGAT 480

QY 161 AsnAsnTrpTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 DB 481 AATAATACATCTGGGGTATCATTTTACTAGCAATCCCAATTCATCTCC 531

RESULT 3
 US-10-218-547-39
 ; Sequence 39, Application US/10218547
 ; Publication No. US20030100074A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Human Genome Sciences, Inc.
 ; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Methods and Compositions for Treating Metabolic Bone Diseases Rel
 ; FILE REFERENCE: PF561
 ; CURRENT APPLICATION NUMBER: US/10/218,547
 ; CURRENT FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: 60/312,542
 ; PRIOR FILING DATE: 2001-08-16
 ; PRIOR APPLICATION NUMBER: 60/330,761
 ; PRIOR FILING DATE: 2001-10-30
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 39
 ; LENGTH: 534

TYPE: DNA
ORGANISM: human
US-10-218-547-39

Alignment Scores:

Pred. No.:	3, 93e-120	Length:	534
Score:	951.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-195-368-1 (1-177) x US-10-218-547-39 (1-534)

```

QY 1 MetCysleuSerHisleuGluAsnMetProleuSerHisSerArgThrGlnGlyAlaGln 20
    1 ATGTGTTGAGCCACTTGGAATAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 60
DB 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
    61 AGATCATCTCGAAGCTGTGGCTCTTTGCTCAATGATTATGTTGCTATTTCTTGCTCC 120
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGlnProCysMetAla 60
    121 TTCAGTTGGCTAACTTTATTTTCTCCATTAGAGACTGCTAAGAGCCCTGTATGGCT 180
DB 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGlnProProCysValAsn 80
    181 AAGTTTGACCATTAACCTCAAAATGGCAATGGCAATGTCATCTTGAACCTCTTGCTGAT 240
QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrlleuIleTyrlGln 100
    241 AAGGTGTGCTGCTGAGAGCTGAGATCTTCAGATGGCTTATATTATTTATTTATGGCAA 300
DB 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGlnValArgLeuTyrlAsn 120
    301 GTGGCTCCCAATGCAAACTCAAAATGAGTAGCTCTTTTAAAGTGGCGGTGTAAATAAC 360
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTy 140
    361 AATAACATGATACAACTCAACAACTCAAAATCAAAATGATAGAGGAGGACTTAT 420
DB 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGlnHisGlnValLeuLys 160
    421 GAATTCGATGTGGGAGACCATGACTGATATCAACTCTGAGCACTGAGGTTCTAAAA 480
QY 161 AsnAsnThrTyrlTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
    481 AATAATACATGCTGGGATATCATTTTACTACCAAAATCCCAATTCACTCTCC 531
DB

```

RESULT 4

US-10-272-328A-9

Sequence 9, Application US/10272328A
Publication No. US20030109444A1

GENERAL INFORMATION:

APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Ross, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFERENCE: 60019620-0206
CURRENT APPLICATION NUMBER: US/10/272,328A
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: 60/329,393
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9

LENGTH: 534

TYPE: DNA

ORGANISM: Homo sapiens

US-10-272-328A-9

Alignment Scores:

Pred. No.:	3, 93e-120	Length:	534
Score:	951.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-195-368-1 (1-177) x US-10-272-328A-9 (1-534)

```

QY 1 MetCysleuSerHisleuGluAsnMetProleuSerHisSerArgThrGlnGlyAlaGln 20
    1 ATGTGTTGAGCCACTTGGAATAATATGCTTTAAGCCATTCAAGAACTCAAGAGCTCAG 60
DB 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
    61 AGATCATCTCGAAGCTGTGGCTCTTTGCTCAATGATTATGTTGCTATTTCTTGCTCC 120
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGlnProCysMetAla 60
    121 TTCAGTTGGCTAACTTTATTTTCTCCATTAGAGACTGCTAAGAGCCCTGTATGGCT 180
DB 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGlnProProCysValAsn 80
    181 AAGTTTGACCATTAACCTCAAAATGGCAATGGCAATGTCATCTTGAACCTCTTGCTGAT 240
QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrlleuIleTyrlGln 100
    241 AAGGTGTGCTGCTGAGAGCTGAGATCTTCAGATGGCTTATATTATTTATTTATGGCAA 300
DB 101 ValAlaProAsnAlaAsnTrpAsnAspValAlaProPheGlnValArgLeuTyrlAsn 120
    301 GTGGCTCCCAATGCAAACTCAAAATGAGTAGCTCTTTTAAAGTGGCGGTGTAAATAAC 360
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTy 140
    361 AATAACATGATACAACTCAACAACTCAAAATCAAAATGATAGAGGAGGACTTAT 420
DB 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGlnHisGlnValLeuLys 160
    421 GAATTCGATGTGGGAGACCATGACTGATATCAACTCTGAGCACTGAGGTTCTAAAA 480
QY 161 AsnAsnThrTyrlTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
    481 AATAATACATGCTGGGATATCATTTTACTACCAAAATCCCAATTCACTCTCC 531
DB

```

RESULT 5

US-10-310-793-43

Sequence 43, Application US/10310793
Publication No. US20030198640A1

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A
APPLICANT: Zhang, Jun
APPLICANT: Wei, Ping
TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Disease
FILE REFERENCE: P573
CURRENT APPLICATION NUMBER: US/10/310,793
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 60/336,695
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 10/226,294
PRIOR FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/314,381
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 09/899,059
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/278,449
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR FILING DATE: 2000-07-07

PRIOR APPLICATION NUMBER: 09/559,290
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR FILING DATE: 1999-05-03
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 71
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 43
LENGTH: 534
TYPE: DNA
ORGANISM: human
US-10-310-793-43

Alignment Scores:

Pred. No.:	3,936-120	Length:	534
Score:	951.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

US-09-195-368-1 (1-177) x US-10-310-793-43 (1-534)

QY 1 MetCysLeuSerHisLeuGluMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
DB 1 AGTGTGTTAGCCACTTGGAATAATAGCTTTAAAGCCATTCAAGAACTCAAGAGAGCTCAG 60
QY 21 ArgSerSerTrpLeuLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
DB 61 AGATCATCTCGAAGCTGGCTCTTTGCTCAATAGTTAGTCTGCTATTTCTTGCTCC 120
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaGlyGluProCysMetAla 60
DB 121 TTCAGTTGGCTATCTTTTCTTCTCCAAATAGAGCTGCTAAGAGAGCCCTGTAAGGCT 180
QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
DB 181 AAGTTTGACATTTACCTCAAAATGGCAATGSCATCTTTCGAACTCTTGCTGCTGAT 240
QY 81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrlGlyGln 100
DB 241 AAGGTGTGCTGAGAGCTGAGATGCTTCAAGATGCTTATATTATTATGSCCAA 300
QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGluValArgLeuTyrlAsn 120
DB 301 GTGGCTCCCAATGCAACTACAAATGATGAGCTCTTTGAGGTGGGCTGTATTAATAAC 360
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrl 140
DB 361 AAAGCATATATCAAACTTACCAAACTTAATAATCCAAATGATGAGAGGAGCTTAT 420
QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
DB 421 GAATGCAAGTTGGGACACCAATGATGATTAATCACTGAGACATCAGGTTCTAAAA 480
QY 161 AsnAsnThrTyrlTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
DB 481 AATAATACATCTGGGGTATCTTTTACTAGCAAAATCCCAATTCATCTCC 531

RESULT 6

US-09-345-790-1
Sequence 1, Application US/09345790
Patent No. US20020099198A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/345,790
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,227
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0470001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 53..559
US-09-345-790-1

Alignment Scores:

Pred. No.:	36-119	Length:	1849
Score:	951.00	Matches:	177
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-195-368-1 (1-177) x US-09-345-790-1 (1-1849)

QY 1 MetCysLeuSerHisLeuGluMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
DB 29 ATGTGTTGACCACTTGGAATAATAGCTTTAAAGCCATTCAAGAACTCAAGAGAGCTCAG 88
QY 21 ArgSerSerTrpLeuLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
DB 89 AGATCATCTCGAAGCTGGCTCTTTGCTCAATAGTTAGTCTGCTATTTCTTGCTCC 148
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGluThrAlaGlyGluProCysMetAla 60
DB 149 TTCAGTTGGCTATCTTTTCTTCTCCAAATAGAGCTGCTAAGAGAGCCCTGTAAGGCT 208
QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGluProProCysValAsn 80
DB 209 AAGTTTGACATTTACCTCAAAATGGCAATGSCATCTTTCGAACTCTTGCTGCTGAT 268
QY 81 LysValSerAspTrpLysLeuGluIleLeuGlnAsnGlyLeuTyrlGlyGln 100
DB 269 AAGGTGTGCTGAGAGCTGAGATGCTTCAAGATGCTTATATTATTATTAATGSCCAA 328
QY 101 ValAlaProAsnAlaSerTrpAsnAspValAlaProPheGlyValArgLeuTyrlAsn 120
DB 329 GTGGCTCCCAATGCAACTACAAATGATGAGCTCTTTGAGAGTGGGCTGTATTAATAAC 388
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyrl 140

DB 389 AAGACATGATACAACTCTAACAACTAAATCCAAATATAGAGGACTTAT 448
QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
DB 449 GAATTCATGTTGGGGACACCATAGACTGATATTAACCTGAGCATCAGGTTCTAAA 508
QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
DB 509 AATAATACCTACTGGGGATCATTTTATAGCAAAATCCCAATTCATCTCC 559

RESULT 7

US-10-136-511-1
Sequence 1, Application US/10136511
Publication No. US20020168729A1
GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
FILE REFERENCE: 1488, 0470007/EKS/PSC
CURRENT APPLICATION NUMBER: US/10/136,511
PRIOR FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/513,584
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/345,790
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 60/136,788
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/122,099
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 08/912,227
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: 60/024,058
PRIOR FILING DATE: 1996-08-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1849
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (53)..(559)
US-10-136-511-1

Alignment Scores:

Pred. No.: 3e-119 Length: 1849
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-195-368-1 (1-177) x US-10-136-511-1 (1-1849)

QY 1 MetCysLeuSerHisIleGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
DB 29 ATGTTGTTGAGCCACTTGAGAAATATGCTTTAAGCCATTCAAGAACTCAAGAGGCTCAG 88
QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
DB 89 AGATCATCTCGAAGCTGTGGCTTTTGTCTCAATATATGTTGCAATTTCTTTGCTCTCC 148
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGluProCysMetAla 60
DB 149 TTCAGTTGGCTAACTTATTTTCTCCAAATAGAGCTCTAAGAGAGCCCTGTATGGCT 208
QY 61 LysPheGlyProLeuProSerLysTrpGlnMetAlaSerSerGlnProProCysValAsn 80
DB 209 AAGTTTGACCATTAACCTCAAAATGCGAAATGSCATCTTGAACCTCCTTGGCGAAT 268
QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyrIleuIleTyrGlyGln 100

DB 269 AAGGCTCTGCTGAACTGGAGATCTTAGATGCTTATATTAAATTATGCGCAA 328
QY 101 ValAlaProAsnAlaAsnTyrAsnAspValAlaProPheGlnValArgLeuTyrLysAsn 120
DB 329 GTGGTCTCCCAATGCAAACTACCAATGATGATGCTCTTTTGGAGTGGCGCTGTAAAAAC 388
QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
DB 389 AAGACATGATACAACTCTAACAACTAAATCCAAATGTAGAGGACTTAT 448
QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
DB 449 GAATTCATGTTGGGGACACCATAGACTGATATTAACCTGAGCATCAGGTTCTAAA 508
QY 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
DB 509 AATAATACCTACTGGGGATCATTTTATAGCAAAATCCCAATTCATCTCC 559

RESULT 8

US-10-080-455-2
Sequence 2, Application US/10080455
Publication No. US20020146389A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Mark, Melanie R.
APPLICANT: Martleters, Scott M.
APPLICANT: Pitti, Robert M.
TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
FILE REFERENCE: P1150R2
CURRENT APPLICATION NUMBER: US/10/080,455
PRIOR FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/195,368
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: US 60/069,661
PRIOR FILING DATE: 1997-12-12
PRIOR APPLICATION NUMBER: US 60/065,635
PRIOR FILING DATE: 1997-11-18
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 1964
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
LOCATION: 1857, 1875
OTHER INFORMATION: n may be any nucleotide
US-10-080-455-2

Alignment Scores:

Pred. No.: 3.31e-119 Length: 1964
Score: 951.00 Matches: 177
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-195-368-1 (1-177) x US-10-080-455-2 (1-1964)

QY 1 MetCysLeuSerHisIleGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
DB 21 ATGTTGTTGAGCCACTTGAGAAATATGCTTTAAGCCATTCAAGAACTCAAGAGGCTCAG 80
QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
DB 81 AGATCATCTCGAAGCTGTGGCTTTTGTCTCAATATATGTTGCAATTTCTTTGCTCTCC 140
QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGluProCysMetAla 60
DB 141 TTCAGTTGGCTAACTTATTTTCTCCAAATAGAGCTCTAAGAGAGCCCTGTATGGCT 200

QY 61 LysPheGlyProLeuProSerIySTpGlnMetAlaSerSerGIuProProCyValAsn 80
 Db 201 AAGTTGACCACTTACCTCCAAATGGCAATGGCATCTTGAACCTCCCTGGGTAAAT 260
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyTyrGlyGln 100
 Db 261 AAGGTGTGACTGAGAGCTGAGATCTGAGATGCTTATATTATTTATTAAGGCCAA 320
 QY 101 ValAlaProAsnAlaAsnTyTyrAsnAspValAlaProPheGluValArgLeuTyTyrLysAsn 120
 Db 321 GTGGCTCCCAATGCACCAATCATATGATGCTCTTTGAGGTGGCGCTGTATATAAAC 380
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
 Db 381 AAGACATGATTCACAACTCTTAACCAACAAATCTAAATCCAAATGTAGAGGAGCTTAT 440
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 441 GAATTCATGTTGGGAGACACCATAGACTGTGATTAATCACTCGAGCATCAGGTCTTAAA 500
 QY 161 AsnAsnThrTyTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
 Db 501 AATAATCACTACTGGGGATTCATTTTACTAGCAATCCCAATTCATCTCC 551

RESULT 9

US-10-116-378-15
 ; Sequence 15, Application US/10116378
 ; Publication No. US2002015093A1
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin
 APPLICANT: Martens, Scot A.
 APPLICANT: Pitti, Robert M.
 APPLICANT: Wood, William
 TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
 TITLE OF INVENTION: NUCLEIC
 FILE REFERENCE: P1206R1
 CURRENT APPLICATION NUMBER: US/10/116,378
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
 NUMBER OF SEQ ID NOS: 31
 SEQ ID NO 15
 LENGTH: 1964
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Unsure
 LOCATION: 1857, 1875
 OTHER INFORMATION: n may be any nucleotide
 US-10-116-378-15

Alignment Scores:

Pred. No.: 3,316-119 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-195-368-1 (1-177) x US-10-116-378-15 (1-1964)

QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20
 Db 21 ATGTGTTGAGCCACTTGAAAAATATGCTTTAAGCCATTCAGAACTCAAGAGAGCTCAG 80
 QY 21 ArgSerSerTrpLysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40

Db 81 AGATCATCTCGAAGCTGTGCTCTTTGCTCAATGATTATGTCATTTCTTTGCTCC 140
 QY 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnTrpAlaLysGluProCysMetAla 60
 Db 141 TTCAGTTGCTAATCTTTATTTTCTCCAAATTAGAGACTGCTAAGAGAGCCCTGATGGCT 200
 QY 61 LysPheGlyProLeuProSerIySTpGlnMetAlaSerSerGIuProProCyValAsn 80
 Db 201 AAGTTGACCACTTACCTCCAAATGGCAATGGCATCTTGAACCTCCCTTGGGTAAAT 260
 QY 81 LysValSerAspTrpLysLeuGlnIleLeuGlnAsnGlyLeuTyTyrGlyGln 100
 Db 261 AAGGTGTGACTGAGAGCTGAGATCTGAGATGCTTATATTATTAATGAGGCCAA 320
 QY 101 ValAlaProAsnAlaAsnTyTyrAsnAspValAlaProPheGluValArgLeuTyTyrLysAsn 120
 Db 321 GTGGCTCCCAATGCACCAATCATATGATGCTCTTTGAGGTGGCGCTGTATATAAAC 380
 QY 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyGlyThrTyr 140
 Db 381 AAGACATGATTCACAACTCTTAACCAACAAATCTAAATCCAAATGTAGAGGAGCTTAT 440
 QY 141 GluLeuHisValGlyAspThrIleAspLeuIlePheAsnSerGluHisGlnValLeuLys 160
 Db 441 GAATTCATGTTGGGAGACACCATAGACTGTGATTAATCACTCGAGCATCAGGTCTTAAA 500

RESULT 10

US-10-116-378-27/c
 ; Sequence 27, Application US/10116378
 ; Publication No. US2002015093A1
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Goddard, Audrey
 APPLICANT: Gurney, Austin
 APPLICANT: Martens, Scot A.
 APPLICANT: Pitti, Robert M.
 APPLICANT: Wood, William
 TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
 TITLE OF INVENTION: NUCLEIC
 FILE REFERENCE: P1206R1
 CURRENT APPLICATION NUMBER: US/10/116,378
 PRIOR FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
 PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
 NUMBER OF SEQ ID NOS: 31
 SEQ ID NO 27
 LENGTH: 1964
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: Unsure
 LOCATION: 90, 108
 OTHER INFORMATION: n may be any nucleotide
 US-10-116-378-27

Alignment Scores:

Pred. No.: 3,316-119 Length: 1964
 Score: 951.00 Matches: 177
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-195-368-1 (1-177) x US-10-116-378-27 (1-1964)

QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgThrGlnGlyAlaGln 20

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Db 1944 ATGTGTTGAGCCACTGGAAATATGCTTTAAGCATTCAAGAACTAAGAGCTCAG 1885
Qy 21 ArgSerSerTrpIysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db 1884 AGATCATCCCGAAGGCTGCTCTTTTGCTCAATGATTATGTGCTATTCTTTGCTCC 1825
Qy 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaIysGlnProCysMetAla 60
Db 1824 TTGAGTGGCTAATCTTATTATTTCTCCCAATTAGACAGCTAAGAGCCCTGTATGGCT 1765
Qy 61 LysPheGlyProLeuProSerIleTyrGlnMetAlaSerSerGlnProProCysValIle 80
Db 1764 AAGTTTGACCACTTACCTCAAAATGGCAATGGCATCTTTCGAACCTCTTGCGGAAAT 1705
Qy 81 LysValSerAspTrpIysLeuGlnIleLeuGlnAsnGlyLeuTyrLeuIleTyrGln 100
Db 1704 AAGGTGCTGACCTGAGAGCTGAGATACCTCAGAAATGCTTATATTATTAATGAGCCAA 1645
Qy 101 ValAlaProSerAlaAsnTyrAsnAspValAlaProPheGlnValArgLeuTyrIysAsn 120
Db 1644 GTGGCTCCCAATGCAATCAATCAATGATGATGCTCTTTGAGGTGGCTGTNTAAATC 1585
Qy 121 LysAspMetIleGlnThrLeuThrAsnLysSerLysIleGlnAsnValGlyIleTyr 140
Db 1584 AAAGACATGATACAACTCAACAACTCAAAATCAAAATGATAGAGGACTAT 1525
Qy 141 GlnLeuHisValAlaGlyAspTrpIleAspLeuIlePheAsnSerGlnIleGlnValLeuIys 160
Db 1524 GAATGTGATGTGGGACACCATGACCTGATGATTAACCTGAGATCAAGGCTCAAAA 1465
Qy 161 AsnAsnThrTyrTrpGlyIleIleLeuLeuAlaAsnProGlnPheIleSer 177
Db 1464 AATTAATACATACCTGGGCTATCACTTTACTAGCAAAATCCCAATTCATCTCC 1414

RESULT 11
US-09-864-761-32533
; Sequence 32533, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2000-09-27

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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32533
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031599.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: NT HIT: G111428077, EVALUATE 7.00e-83
; OTHER INFORMATION: SWISSPROT HIT: P25003, EVALUATE 1.30e+00
; OTHER INFORMATION: EST_HUMAN HIT: A1636075.1, EVALUATE 9.60e-02
US-09-864-761-32533

Alignment Scores:
Score: 3.07e-29 Length: 162
Percent Similarity: 281.00 Matches: 52
Best Local Similarity: 100.00% Conservative: 0
Query Match: 100.00% Mismatches: 0
De: 29.55% Indels: 0
Gaps: 0

US-09-195-368-1 (1-177) x US-09-864-761-32533 (1-162)

Qy 1 MetCysLeuSerHisLeuGlnAsnMetProLeuSerHisSerArgThrGlnIleGln 20
Db 1 ATGTGTTGAGCCACTGGAAATATGCTTTAAGCATTCAAGAACTAAGAGCTCAG 60
Qy 21 ArgSerSerTrpIysLeuTrpLeuPheCysSerIleValMetLeuLeuPheLeuCysSer 40
Db 61 AGATCATCCCGAAGGCTGCTCTTTTGCTCAATGATTATGTGCTATTCTTTGCTCC 120
Qy 41 PheSerTrpLeuIlePheIlePheLeuGlnLeuGlnThrAlaIysGlnProCysMetAla 52
Db 121 TTGAGTGGCTAATCTTATTATTTCTCCCAATTAGAG 156

RESULT 12
US-09-864-761-16032
; Sequence 16032, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16032
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031599.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
US-09-864-761-16032

Alignment Scores:
Pred. No.: 2,1e-13 Length: 397
Score: 170.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 17.88% Indels: 0
DB: 9 Gaps: 0

US-09-195-368-1 (1-177) x US-09-864-761-16032 (1-397)
QY 1 MetCysLeuSerHisLeuGluAsnMetProLeuSerHisSerArgTrpGlnGlyAlaGln 20
DB 307 ATGTGTTGAGCCACTTGGAATAATGCTTTAAGCCATTCAAGACTCAAGAGCTCAG 366
QY 21 ArgSerSerTrpGlyLeuTrpLeuPheCys 30
DB 367 AGATCATCTCTGGAAGCTGTGCTCTTTGC 396

RESULT 13
US-09-908-975-14130
; Sequence 14130, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FAIGLER, Simcha
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28

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; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14130
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-14130

Alignment Scores:
Pred. No.: 4.03e-06 Length: 60
Score: 107.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.25% Indels: 0
DB: 10 Gaps: 0

US-09-195-368-1 (1-177) x US-09-908-975-14130 (1-60)
QY 72 AlaSerSerGluProCysValAsnGlyValSerAspTrpGlyLeuGluLeuGln 91
DB 1 GCATCTTCTGAACTCTCTGCGTGAATAAGTGTGACTGGAAGCTGAGATCTTCTCAG 60

RESULT 14
US-10-131-827-2732
; Sequence 2732, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Noblgenmuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2732
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-2732

Alignment Scores:
Pred. No.: 0.000339 Length: 50
Score: 92.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.67% Indels: 0
DB: 15 Gaps: 0

US-09-195-368-1 (1-177) x US-10-131-827-2732 (1-50)
QY 151 IlePheAsnSerGluHisGlnValLeuGlyAsnAsnThrTrpGly 166
DB 3 ATATTCAACTCTGAGCATCAGGTTCTAAAAAATATACATACCTGGGCT 50

RESULT 15
US-10-027-632-287892/C
; Sequence 287892, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30

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/ PRIOR APPLICATION NUMBER: US 60/218,006
 / PRIOR FILING DATE: 2000-07-12
 / PRIOR APPLICATION NUMBER: US 60/198,676
 / PRIOR FILING DATE: 2000-04-20
 / PRIOR APPLICATION NUMBER: US 60/193,483
 / PRIOR FILING DATE: 2000-03-29
 / PRIOR APPLICATION NUMBER: US 60/185,218
 / PRIOR FILING DATE: 2000-02-24
 / PRIOR APPLICATION NUMBER: US 60/167,363
 / PRIOR FILING DATE: 1999-11-23
 / PRIOR APPLICATION NUMBER: US 60/156,358
 / PRIOR FILING DATE: 1999-09-28
 / PRIOR APPLICATION NUMBER: US 60/146,002
 / PRIOR FILING DATE: 1999-08-09
 / NUMBER OF SEQ ID NOS: 325720
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 287892
 / LENGTH: 686
 / TYPE: DNA
 / ORGANISM: Human
 / US-10-027-632-287892

Alignment Scores:
 Pred. No.: 0.087 Length: 686
 Score: 88.00 Matches: 29
 Percent Similarity: 45.26% Conservative: 14
 Best Local Similarity: 30.53% Mismatches: 31
 Query Match: 9.25% Indels: 23
 DB: 15 Gaps: 4

US-09-195-368-1 (1-177) x US-10-027-632-287892 (1-686)

QY 5 HisLeuGluAsnMetProLeuSerHisSerArg-----Thr 16
 DB 558 CATTGAGAAAGTATCTCTCCGCGCAGTACGACAAAGCCACAGATTATGAAAGAG 499
 QY 17 GlnGlyAlaGlnArgSerSerTyrLeuTyrLeuPheCysSerIleValMetLeu 36
 DB 498 GAAGGAGGACAGAACTGGRCAGAGTTCTGG---TTTGTTCCTGTATTGTTG--- 445
 QY 37 PheLeuCysSerSerPheLeuIlePheIlePheLeuGlnLeuGlnThrAlaLysGlu 56
 DB 444 -----TCATTGTACTGTTGTTTCTTTT-TTGAGACAGAGTCTCGC 401
 QY 57 ProCysMetAlaLysPheGlyProLeuProSerIleTyrGlnMetAlaSerSerGluPro 76
 DB 400 ACTTGTCCTCCAGCAGAGATGCAATGCGCAGCTTGGCTCAGCTCAACCTCCA--CCT 343
 QY 77 Pro-----CysValAsnLysValSerAspTyr 85
 DB 342 CCGAGCTTCAAGGAGATTCTCTGCTCGAGCTCTCGAGTACCTGG 298

Search completed: April 8, 2004, 04:20:17
 Job time : 301.896 secs